

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 13, 2004, 14:34:12 ; Search time 193 Seconds  
(without alignments)  
193.779 Million cell updates/sec

Title: US-10-272-121-2

Perfect score: 357

Sequence: 1 MRHYLLFALLFLFLVFPVG.....LPKEEQIKGKSTRGRKCCR 65

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 segs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_02:\*

1: uniprot\_sprot:\*

2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	357	100.0	67	1	D103_HUMAN	P81534 homo sapien
2	353	98.9	67	2	Q7PCK4	Q7pck4 papio anubi
3	349	97.8	64	1	D103_PANTR	Q95jd2 pan troglod
4	302	84.6	67	1	BD01_CHILA	P83943 chinchilla
5	298	83.5	67	2	Q6SC68	Q6sc68 sus scrofa
6	298	83.5	67	2	AAR88759	Aar88759 sus scrof
7	256	71.7	67	2	Q7TNV9	Q7tnv9 mus musculu
8	143	40.1	64	2	Q865P6	Q865p6 equus cabal
9	135	37.8	64	1	BD02_PANTR	Q9bt12 pan troglod
10	134	37.5	64	1	BD02_MACMU	Q9bds9 macaca mula
11	133	37.3	64	1	BD02_HUMAN	O15263 homo sapien
12	133	37.3	64	2	AAH65285	Aah65285 homo sapi
13	116.5	32.6	63	1	BD03_MOUSE	Q9wt10 mus musculu
14	116	32.5	64	1	EAP_BOVIN	O02775 bos taurus
15	115	32.2	60	2	Q71U45	Q71u45 bos taurus
16	115	32.2	60	2	AAD43032	Aad43032 bos tauru
17	114	31.9	64	1	BD01_PIG	O62697 sus scrofa
18	108	30.3	64	1	LAP_BOVIN	Q28880 bos taurus
19	108	30.3	65	1	MYX1_CRODU	P24331 croctalus du
20	108	30.3	65	1	MYX3_CRODU	P24333 croctalus du
21	106	29.7	64	1	BD05_BOVIN	P46163 bos taurus
22	106	29.7	64	1	TAP_BOVIN	P25068 bos taurus
23	105	29.4	65	2	Q9PWF3	Q9pwf3 croctalus du
24	103	28.9	65	2	O57540	O57540 croctalus du
25	102	28.6	71	2	Q91V70	Q91v70 mus musculu
26	101	28.3	63	2	Q6TWH5	Q6twh5 bubalus bub
27	101	28.3	63	2	AAQ93463	Aaq93463 bubalus b
28	101	28.3	64	2	Q7YS43	Q7yb43 bubalus bub
29	100	28.0	64	2	O97942	O97942 capra hircu
30	96.5	27.0	80	2	Q9DG58	Q9dg58 galus galli
31	96	26.9	64	2	O73799	O73799 croctalus du

## ALIGNMENTS

32	95.5	26.8	63	1	BD02_RAT	O88514 rattus norv
33	95	26.6	64	1	BD01_CAPHI	O97946 capra hircu
34	95	26.6	64	1	BD02_SHEEP	O19039 ovis aries
35	94	26.3	53	1	BD07_BOVIN	O18815 bos taurus
36	94	26.3	64	2	Q9EPV9	Q9epv9 mus musculu
37	93.5	26.2	63	2	Q91VD6	Q91vd6 mus musculu
38	93.5	26.2	80	2	Q6GXJ2	Q6gxj2 gallus gall
39	93	26.1	60	2	Q8R556	Q8r556 mus musculu
40	92	25.8	60	2	Q91V82	Q91v82 mus musculu
41	92	25.8	63	1	BD04_BOVIN	P46162 bos taurus
42	90.5	25.4	63	1	BD04_MOUSE	P82019 mus musculu
43	89.5	25.1	59	2	Q9DG57	Q9dg57 meleagris g
44	89	24.9	42	1	BD06_BOVIN	P46164 bos taurus
45	89	24.9	69	1	BD01_RAT	O89117 rattus norv

RESULT 1  
ID D103\_HUMAN STANDARD; PRT; 67 AA.  
AC P81534; Q8NFG6; Q9NPF6;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 01-OCT-2004 (Rel. 45, Last annotation update)  
DE Beta-defensin 103A precursor (Beta-defensin 3) (DEFB-3) (BD-3) (hBD-3)  
DE (HBD3) (Defensin like protein).  
GN Name=DEFB103A; Synonyms=DEFB103, DEFB3, BD3;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A., SEQUENCE OF 23-67, FUNCTION, TISSUE SPECIFICITY,  
RP INDUCTION, AND MASS SPECTROMETRY.  
RC TISSUE=Keratinocytes, lung epithelial cells, and Tracheal epithelium;  
RX MEDLINE=21101950; PubMed=11085990; DOI=10.1074/jbc.M008557200;  
RA Harder J., Bartels J., Christophers E., Schroeder J.-M.;  
RT "Isolation and characterization of human beta-defensin-3, a novel  
RT human inducible peptide antibiotic."  
RL J. Biol. Chem. 276:5707-5713(2001).  
RN [2]  
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.  
RX MEDLINE=2158153; PubMed=11702237; DOI=10.1007/s004410100433;  
RA Conejo-Garcia J.-R., Jaumann F., Schulz S., Krause A.,  
RA Rodriguez-Jimenez J., Forssmann U., Adermann K., Kluever E.,  
RA Vogelemeier C., Becker D., Hedrich R., Forssmann W.-G., Bals R.;  
RT "Identification of a novel, multifunctional beta-defensin (human beta-  
RT defensin 3) with specific antimicrobial activity. Its interaction with  
RT plasma membranes of Xenopus oocytes and the induction of macrophage  
RT chemotactic action."  
RL Cell Tissue Res. 306:257-264(2001).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21125233; PubMed=11223260; DOI=10.1016/S0378-1119(00)00569-2;  
RA Jia H.P., Schutte B.C., Schudy A., Linzmeier R., Guthmiller J.M.,  
RA Johnson G.K., Tack B.F., Mitros J.P., Rosenthal A., Ganz T.,  
RA McCrory P.B. Jr.;  
RT "Discovery of new human defensins using a genomics-based approach."  
RL Gene 263:211-218(2001).  
RN [4]  
RP SEQUENCE FROM N.A.  
RA Imai Y.;  
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.  
RN [5]  
RP SEQUENCE FROM N.A.  
RA Adler D.A., Diamond G., Sheppard P., Holloway J., Presnell S.,  
RA Jaepers S., Whitmore T., Fox B., Gosink J., Rixon M., Gao Z.,  
RA Haldeman B., O'Hara P.;  
RT "EST and genomic database mining yield novel human and mouse beta-  
RT defensins."  
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.

RN [6]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Tonsil;  
RA Chen S., He F., Li R.;  
RT "Cloning and expression of Chinese human beta defensin-3."  
RU Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.  
RN [7]  
RP STRUCTURE BY NMR OF 23-67.  
RX MEDLINE=21864161; PubMed=11741980; DOI=10.1074/jbc.M108830200;  
RA Schibli D.J., Hunter H.N., Aseyev V., Starnier T.D., Wiencek J.M.,  
RA McCray P.B. Jr., Jack B.F., Vogel H.J.;  
RT "The solution structures of the human beta-defensins lead to a better  
RT understanding of the potent bactericidal activity of HBD3 against  
RT Staphylococcus aureus";  
RU J. Biol. Chem. 277:8279-8289 (2002).  
CC -1- FUNCTION: Exhibits antimicrobial activity against Gram-positive  
CC bacteria S.aureus and S.pyogenes, Gram-negative bacteria  
CC P.aeruginosa and E.coli and the yeast C.albicans. Kills  
CC multi-resistant S.aureus and vancomycin-resistant E.faecium. No  
CC significant hemolytic activity was observed.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- TISSUE SPECIFICITY: Highly expressed in skin and tonsils, and to a  
CC lesser extent in trachea, uterus, kidney, thymus, adenoid, pharynx  
CC and tongue. Low expression in salivary gland, bone marrow, colon,  
CC stomach, polyp and larynx. No expression in small intestine.  
CC -1- INDUCTION: By infection of bacteria and by interferon gamma.  
CC -1- MASS SPECTROMETRY: MW=5154.59; METHOD=Electrospray; RANGE=23-67;  
CC NOTE=Ref.1.  
CC -1- SIMILARITY: Belongs to the beta-defensin family.  
CC  
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CC  
-----  
DR EMBL; AJ237673; CAC03097.1; -;  
DR EMBL; AF295370; AAG02237.1; -;  
DR EMBL; AF217245; AAF73853.1; -;  
DR EMBL; AB037972; BAB40572.1; -;  
DR EMBL; AF301470; AAG22030.1; -;  
DR EMBL; AF516673; AAM62424.1; -;  
DR PDB; 1KJ6; NMR; A=23-66.  
DR GeneW; HGNC:15967; DEFBI03A.  
DR MIM; 606611; -;  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0006965; P:anti-Gram-positive bacterial polypeptide in. . .; TAS.  
DR InterPro; IPR001855; Defensin\_beta.  
DR Pfam; PF00711; Defensin\_beta; 1.  
DR 3D-structure; Antibiotic; Direct protein sequencing; Signal.  
FT SIGNAL 1 22  
FT CHAIN 23 67 Beta-defensin 103A.  
FT DISULFID 33 62  
FT DISULFID 40 55  
FT DISULFID 45 63  
FT DISULFID 45 63  
FT CONFLICT 29 31 C -> R (in Ref. 6).  
FT TURN 29 31  
FT HELIX 32 36  
FT STRAND 39 41  
FT TURN 47 48  
FT STRAND 49 53  
FT STRAND 61 65  
SQ SEQUENCE 67 AA; 7697 MW; 54266DE1C90D4B65 CRC64;  
Query Match 100.0%; Score 357; DB 1; Length 67;  
Best Local Similarity 100.0%; Pred. No. 6.5e-34;  
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MRIHYLLFALLFLVLPVPGHGIIINTLOKYYCRVGRGRCAYLSCLPKKEQIGKSTRGR 60  
Db 1 MRIHYLLFALLFLVLPVPGHGIIINTLOKYYCRVGRGRCAYLSCLPKKEQIGKSTRGR 60

QY 61 KCCR 65  
Db 61 KCCR 65  
RESULT 2  
Q7PCK4 PRELIMINARY; PRT; 67 AA.  
AC Q7PCK4;  
DT 01-MAR-2004 (TREMBLrel. 26, Created)  
DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)  
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
DE DEFBI03-like protein (Fragment).  
OS Papio anubis (Olive baboon).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
OC Cercopithecinae; Papio.  
OX NCBI\_TaxID=9555;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22619651; PubMed=12734011;  
RA Sempke C.A., Rolfe M., Dorin J.R.;  
RT "Duplication and selection in the evolution of primate beta-defensin  
RT genes";  
RU Genome Biol. 4:R31-R31(2003).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Sempke C.A.M., Rolfe M., Dorin J.R.;  
RU Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.  
CC -1- MISCELLANEOUS: The sequence shown here is derived from an  
CC EMBL/GenBank/DBJ third party annotation (TPA) entry.  
DR EMBL; BK000557; DAA01350.1; -;  
DR GO; GO:0005576; C:extracellular; IEA.  
DR GO; GO:0006952; P:defense response; IEA.  
DR GO; GO:0009613; P:response to pest/pathogen/parasite; IEA.  
DR InterPro; IPR001855; Defensin\_beta.  
DR Pfam; PF00711; Defensin\_beta; 1.  
DR NON\_TER 67  
FT SEQUENCE 67 AA; 7669 MW; 543F50570B5D4B65 CRC64;  
SQ SEQUENCE 67 AA; 7669 MW; 543F50570B5D4B65 CRC64;  
Query Match 98.9%; Score 353; DB 2; Length 67;  
Best Local Similarity 98.5%; Pred. No. 1.9e-33;  
Matches 64; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 MRIHYLLFALLFLVLPVPGHGIIINTLOKYYCRVGRGRCAYLSCLPKKEQIGKSTRGR 60  
Db 1 MRIHYLLFALLFLVLPVPGHGIIINTLOKYYCRVGRGRCAYLSCLPKKEQIGKSTRGR 60  
QY 61 KCCR 65  
Db 61 KCCR 65  
RESULT 3  
D103\_PANTR STANDARD; PRT; 64 AA.  
ID D103\_PANTR  
AC Q95JD2;  
DT 29-MAR-2004 (Rel. 43, Created)  
DT 29-MAR-2004 (Rel. 43, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Beta-defensin 103A precursor (Beta-defensin 3) (DEFB-3) (BD-3)  
DE (Fragment).  
GN Name=DEFBI03A; Synonyms=DEFBI03, DEFB3;  
OS Pan troglodytes (Chimpanzee).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Pan.  
OX NCBI\_TaxID=9598;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Skin;  
RA Dults L.A., Langermans J.A.M., Ravensbergen B., Paltansing S.,  
RA Vervenne R.A.W., Hiemstra P.S., Thomas A.W., Nibbering P.H.;

```
RT "Expression of chimpanzee (Pan troglodytes) beta-defensin-3." ;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Exhibits antimicrobial activity against Gram-positive
CC and Gram-negative bacteria (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the beta-defensin family.
CC -----
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CC -----
DR EMBL; AY033883; AAK61549.1; -.
DR InterPro; IPR001855; Defensin_beta.
DR Pfam; PF00711; Defensin_beta.1.
KW Antibiotic; Signal.
FT SIGNAL 1 22 By similarity.
FT CHAIN 1 22 Beta-defensin 103A.
FT DISULFID 33 62 By similarity.
FT DISULFID 40 55 By similarity.
FT DISULFID 45 63 By similarity.
FT NON TER 64 64
SQ SEQUENCE 64 AA; 7299 MW; 01C90D4B60218DC8 CRC64;

Query Match 97.8%; Score 349; DB 1; Length 64;
Best Local Similarity 98.4%; Pred. No. 5.3e-33;
Matches 63; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRIHYLLFALLFLFVLPVPGHGIIINTLQKYCRVGRCAVLSCLPKKEQIGKSTRGR 60
DB 1 MRIHYLLFALLFLFVLPVPGHGIIINTLQKYCRVGRCAVLSCLPKKEQIGKSTRGR 60

QY 61 KCCR 64
DB 61 KCCR 64

RESULT 4
ID BD01_CHILA STANDARD; PRT; 67 AA.
AC P83943;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DE Beta-defensin 1 precursor (CBD-1).
GN Name=DEFB1; Synonyms=BD1;
OS Chinchilla lanigera (Chinchilla).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriognathi; Chinchillidae;
OC Chinchilla.
OX NCBI_TaxID=34839;
RN [1]
RP SEQUENCE FROM N.A., FUNCTION, TISSUE SPECIFICITY, AND MASS
RP SPECTROMETRY.
RC TISSUE=Tongue, and Trachea;
RX PubMed=14996845; DOI=10.1074/jbc.M400499200;
RA Harris R.H., Wilk D., Bevins C.L., Munson R.S. Jr., Bakaletz L.O.;
RT "Identification and characterization of mucosal antimicrobial peptides
RT expressed by the chinchilla (Chinchilla lanigera) airway.";
RL J. Biol. Chem. 279:20250-20256(2004).
CC -!- FUNCTION: Has antibacterial activity against Gram-positive
CC bacterium S.pneumoniae serotype 14. Is also active against Gram-
CC negative bacteria M.cattarrhalis 1857, and nontypeable H.influenzae
CC strains 86-028NP and 1128. Has antifungal activity against
CC C.albicans. May have a role in maintaining sterility in the middle
CC ear.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Highly expressed in tongue, nasopharyngeal
CC mucosa and skin, and to a lower extent in the Eustachian tube,
CC lung and trachea.
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CC -!- MASS SPECTROMETRY: MW=5123; METHOD=Electrospray; RANGE=23-67;
CC NOTE=Ref.1.
CC -!- SIMILARITY: Belongs to the beta-defensin family.
CC -----
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CC -----
DR EMBL; AY128668; AAM97293.1; -.
DR InterPro; IPR006080; Defensin_mammal.
DR SMART; SM00048; DEFSN; 1.
KW Antibiotic; Fungicide; Signal.
FT SIGNAL 1 22 Potential.
FT CHAIN 1 22 Beta-defensin 1.
FT DISULFID 33 62 By similarity.
FT DISULFID 40 55 By similarity.
FT DISULFID 45 63 By similarity.
SQ SEQUENCE 67 AA; 7676 MW; 30A611CDDC5BA8D CRC64;

Query Match 84.6%; Score 302; DB 1; Length 67;
Best Local Similarity 79.7%; Pred. No. 1.7e-27;
Matches 51; Conservative 9; Mismatches 4; Indels 0; Gaps 0;

QY 1 MRIHYLLFALLFLFVLPVPGHGIIINTLQKYCRVGRCAVLSCLPKKEQIGKSTRGR 60
DB 1 MRIHYLLFALLFLFVLPVPGHGIIINTLQKYCRVGRCAVLSCLPKKEQIGKSTRGR 60

QY 61 KCCR 64
DB 61 KCCR 64

RESULT 5
ID Q6SC68 PRELIMINARY; PRT; 67 AA.
AC Q6SC68;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Prepro-beta-defensin 3.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Sang Y., Zhang G., Ross C.R., Blecha F.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY460575; AAR88759.1; -.
SQ SEQUENCE 67 AA; 7790 MW; 6BC28264846572AC CRC64;

Query Match 83.5%; Score 298; DB 2; Length 67;
Best Local Similarity 80.0%; Pred. No. 4.9e-27;
Matches 52; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

QY 1 MRIHYLLFALLFLFVLPVPGHGIIINTLQKYCRVGRCAVLSCLPKKEQIGKSTRGR 60
DB 1 MRIHYLLFALLFLFVLPVPGHGIIINTLQKYCRVGRCAVLSCLPKKEQIGKSTRGR 60

QY 61 KCCR 65
DB 61 KCCR 65

RESULT 6
ID AAR88759 PRELIMINARY; PRT; 67 AA.
AC AAR88759;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
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DT 02-MAR-2004 (TREMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TREMBLrel. 27, Last annotation update)
DE Prepro-beta-defensin 3.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Sang Y., Zhang G., Ross C.R., Blecha F.;
RT "Characterization of porcine beta-defensin 3 and synergistic effect of
RL porcine beta-defensin 1, 2 and 3."
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY460575; AAR88759.1;
SQ SEQUENCE 67 AA; 7790 MW; 6BC28264846572AC CRC64;

Query Match
Best Local Similarity 83.5%; Score 298; DB 2; Length 67;
Matches 52; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

QY 1 MRIHYLLFALLFLVVPVPGHGIINTLQKYYCVRGRCAYLSCLPKEQIGKSTRGR 60
DB 1 MRIHYLLFALLFLVFPGLPGRRIINTLQRYCKIRGRCAVLCGLPKKEQIGSCSVSGR 60

QY 61 KCCRR 65
DB 61 KCCRK 65
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RESULT 7
Q7TNV9 PRELIMINARY; PRT; 67 AA.
ID Q7TNV9
AC Q7TNV9;
DT 01-OCT-2003 (TREMBLrel. 25, Created)
DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Beta defensin 14.
GN Name=Defb14;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Maxwell A.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Dorin J.R.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ578468; CAB17665.2;
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR GO; GO:0009613; P:response to pest/pathogen/parasite; IEA.
DR InterPro; IPR001855; Defensin_beta.
DR Pfam; PF00711; Defensin_beta; 1.
SQ SEQUENCE 67 AA; 7718 MW; EEF0D93ADF17452 CRC64;

Query Match
Best Local Similarity 71.7%; Score 256; DB 2; Length 67;
Matches 44; Conservative 9; Mismatches 12; Indels 0; Gaps 0;

QY 1 MRIHYLLFALLFLVVPVPGHGIINTLQKYYCVRGRCAYLSCLPKEQIGKSTRGR 60
DB 1 MRIHYLLFALLFLVVPVPGHGIINTLQKYYCVRGRCAYLSCLPKEQIGKSTRGR 60

QY 61 KCCRR 65
DB 61 KCCRK 65
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RESULT 8
Q865P6 PRELIMINARY; PRT; 64 AA.
ID Q865P6
AC Q865P6;
DT 01-JUN-2003 (TREMBLrel. 24, Created)
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Beta-defensin-1.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RA Sang Y., Davis E.G., Blecha F.;
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY170305; AA032801.1;
DR HSSP; P46170; 1BNB.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR GO; GO:0009613; P:response to pest/pathogen/parasite; IEA.
DR InterPro; IPR006080; Defensin_mammal.
DR SMART; SM00048; DEFSN; 1.
SQ SEQUENCE 64 AA; 6876 MW; 58C016282PBB4914 CRC64;

Query Match
Best Local Similarity 40.1%; Score 143; DB 2; Length 64;
Matches 30; Conservative 6; Mismatches 27; Indels 2; Gaps 1;

QY 1 MRIHYLLFALLFLVVPVPGHGIINTLQKYYCVRGRCAYLSCLPKEQIGKSTRGR 60
DB 1 MRIHYLLFALLFLVFPVPGTAGIET--SFSCSNGGFCISPKCLPGSKQIGTCLLPGS 58

QY 61 KCCRR 65
DB 59 KCCRK 63
```

```
RESULT 9
BD02_PANTR STANDARD; PRT; 64 AA.
ID BD02_PANTR
AC Q9T12;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Beta-defensin 2 precursor (BD-2) (Defensin, beta 2).
GN Name=DEFB4; Synonyms=DEFB2, DEFB102;
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RA Duits L.A., Langermans J.A.M., van der Straaten T., Vervene R.A.W.,
RA Paltansing S., Frost P.A., Hiemstra P.S., Thomas A.W., Nibbering P.H.;
RT "Expression of beta-defensin-2 in chimpanzee (Pan troglodytes).";
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Has antibacterial activity (Potential).
CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
CC -1- SIMILARITY: Belongs to the beta-defensin family. LAP/TAP
subfamily.
CC -----
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CC -----
CC EMBL; AF209855; AAF20154.1; -.
CC HSSP; O15263; IE4Q.
CC InterPro; IPR001855; Defensin_beta.
```



DR Pfam: PF00711; Defensin\_beta; 1.  
KW Antibiotic; Signal.  
FT SIGNAL 1 23 Potential.  
FT CHAIN 24 64 Beta-defensin 2.  
FT DISULFID 31 60 By similarity.  
FT DISULFID 38 53 By similarity.  
FT DISULFID 43 61 By similarity.  
SQ SEQUENCE 64 AA; 7068 MW; B0D2454CE7ACCD13 CRC64;  
  
Query Match 37.8%; Score 135; DB 1; Length 64;  
Best Local Similarity 42.4%; Pred. No. 4.9e-08;  
Matches 28; Conservative 12; Mismatches 22; Indels 4; Gaps 2;  
  
QY 1 MRIHYLLFALLFLFVPG-HGGIINTLQKYYCRVGRCAVLSCLPKKEQIGKSTRG 59  
Db 1 MRVLYLFSFLFILMPGVFGISDPVT---CLKSGAICHVPFCPRRYKQIGTCGLPG 57  
  
QY 60 RKCCR 65  
Db 58 TKCCKK 63  
  
RESULT 10  
BD02\_MACMU STANDARD; PRT; 64 AA.  
ID BD02\_MACMU  
AC Q9BDS9;  
DT 05-JUL-2004 (Rel. 44, Created)  
DT 05-JUL-2004 (Rel. 44, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Beta-defensin 2 precursor (BD-2) (RhBD-2) (Defensin, beta 2).  
GN Name=DEFB4; Synonyms=DEFB2;  
OS Macaca mulatta (Rhesus macaque).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;  
OC Cercopitheciinae; Macaca.  
OX NCBI\_TaxID=9544;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX PubMed=11238224; DOI=10.1128/CDLI.8.2.370-375.2001;  
RA Bals R., Lang C., Weiner D.J., Vogelmeier C., Welsch U., Wilson J.M.;  
RT "Rhesus monkey (Macaca mulatta) mucosal antimicrobial peptides are  
RT close homologues of human molecules.";  
RL Clin. Diagn. Lab. Immunol. 8:370-375(2001).  
CC -1- FUNCTION: Has antibacterial activity (Potential).  
CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).  
CC -1- SIMILARITY: Belongs to the beta-defensin family. LAP/TAP  
CC subfamily.  
CC -----  
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CC -----  
CC EMBL; AF288286; AAK26259.1; -.  
DR HSSP; O15263; 1PD3.  
DR InterPro; IPR001855; Defensin\_beta.  
DR InterPro; IPR006080; Defensin\_mammal.  
DR Pfam; PF00711; Defensin\_beta; 1.  
DR SMART; SM00048; DEFSN; 1.  
KM Antibiotic; Signal.  
FT SIGNAL 1 23 Potential.  
FT CHAIN 24 64 Beta-defensin 2.  
FT DISULFID 31 60 By similarity.  
FT DISULFID 38 53 By similarity.  
FT DISULFID 43 61 By similarity.  
SQ SEQUENCE 64 AA; 7065 MW; BB26454CE7ACDDF CRC64;  
  
Query Match 37.5%; Score 134; DB 1; Length 64;  
Best Local Similarity 42.4%; Pred. No. 6.5e-08;  
Matches 28; Conservative 12; Mismatches 22; Indels 4; Gaps 2;

QY 1 MRIHYLLFALLFLFVPG-HGGIINTLQKYYCRVGRCAVLSCLPKKEQIGKSTRG 59  
Db 1 MRVLYLFSFLFILMPGVFGISDPVT---CLKNGAICHVPFCPRRYKQIGTCGLPG 57  
  
QY 60 RKCCR 65  
Db 58 TKCCKK 63  
  
RESULT 11  
BD02\_HUMAN STANDARD; PRT; 64 AA.  
ID BD02\_HUMAN  
AC O15263;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 01-OCT-2004 (Rel. 45, Last annotation update)  
DE Beta-defensin 2 precursor (BD-2) (hBD-2) (Defensin, beta 2) (Skin-  
DE antimicrobial peptide 1) (SAP1).  
GN Name=DEFB4; Synonyms=DEFB2, DEFB102;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Skin;  
RX MEDLINE=97345625; PubMed=9202117;  
RA Harder J., Bartels J.H., Christophers E., Schroeder J.-M.;  
RT "A peptide antibiotic from human skin.";  
RL Nature 387:861-861(1997).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Placenta;  
RX MEDLINE=99051334; PubMed=9831658;  
RA Liu L., Wang L., Jia H.P., Zhao C., Heng H.H.Q., Schutte B.C.,  
RA McCray P.B., Jr., Ganz T.;  
RT "Structure and mapping of the human beta-defensin HBD-2 gene and its  
RT expression at sites of inflammation.";  
RL Gene 222:237-244(1998).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20072673; PubMed=10603376;  
RA Diamond G., Kaiser V., Rhodes J., Russell J.P., Bevins C.L.;  
RT "Transcriptional regulation of beta-defensin gene expression in  
RT tracheal epithelial cells.";  
RL Infect. Immun. 68:113-119(2000).  
RN [4]  
RP SEQUENCE FROM N.A.  
RA Harder J., Schroeder J.-M.;  
RT "Transcriptional regulation of the human beta-defensin-2 (hBD-2).";  
RT Submitted (Aug-1997) to the EMBL/GenBank/DBJ databases.  
RN [5]  
RP SYNTHESIS OF 24-64.  
RX MEDLINE=22007551; PubMed=12010514;  
RA Kluever E., Schulz A., Forssmann W.-G., Adermann K.;  
RT "Chemical synthesis of beta-defensins and LEAP-1/hepcidin.";  
RL J. Pept. Res. 59:241-248(2002).  
RN [6]  
RP X-RAY CRYSTALLOGRAPHY (1.35 ANGSTROMS).  
RX MEDLINE=20490730; PubMed=10906336; DOI=10.1074/jbc.M006098200;  
RA Hoover D.M., Rajashankar K.R., Blumenthal R., Puri A., Oppenheim J.J.,  
RA Chertov O., Lubkowski J.;  
RT "The structure of human beta-defensin-2 shows evidence of higher order  
RT oligomerization.";  
RL J. Biol. Chem. 275:32911-32918(2000).  
RN [7]  
RP STRUCTURE BY NMR OF 28-64.  
RX MEDLINE=21571984; PubMed=11714914;  
RA Bauer F., Schweimer K., Kluever E., Conejo-Garcia J.-R.,  
RA Forssmann W.-G., Rosch P., Adermann K., Sticht H.;  
RT "Structure determination of human and murine beta-defensins reveals  
RT structural conservation in the absence of significant sequence

```
RT similarity."
RL Protein Sci. 10:2470-2479 (2001).
CC -1- FUNCTION: Has antibacterial activity (Potential).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed in the skin and respiratory tract.
CC -1- INDUCTION: By inflammation.
CC -1- SIMILARITY: Belongs to the beta-defensin family. IAP/TAP
      subfamily.
CC -----
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CC -----
DR EMBL; Z71389; CAA95992.1; -.
DR EMBL; AF040153; AAC33549.1; -.
DR EMBL; AF071216; AAC69554.1; -.
DR EMBL; AJ000152; CAB65126.1; -.
DR PDB; 1E4Q; NMR; A=28-64.
DR PDB; 1FD3; X-ray; A/B/C/D=24-64.
DR PDB; 1FD4; X-ray; A/B/C/D/E/F/G/H/I/J/K/L/M/N/O/P=24-64.
DR PDB; 1FQO; NMR; A=24-64.
DR Genew; HGNC:2767; DEFBA4.
DR MIM; 602215; -.
DR GO; GO:0006935; P:chemotaxis; TAS.
DR GO; GO:0007186; P:G-protein coupled receptor protein signaling. . .; TAS.
DR GO; GO:0006955; P:immune response; TAS.
DR GO; GO:0009613; P:response to pest/pathogen/parasite; TAS.
DR InterPro; IPR001855; Defensin_beta.
DR Pfam; PF00711; Defensin_beta; 1.
KM 3D-structure; Antidiotic; Signal.
FT SIGNAL 1 23 Potential.
FT CHAIN 1 64 Beta-defensin 2.
FT DISULFID 31 60
FT DISULFID 38 53
FT DISULFID 43 61
FT STRAND 25 26
FT STRAND 28 33.
FT HELIX 34 35
FT TURN 37 39
FT STRAND 45 46
FT STRAND 48 52
FT TURN 56 57
FT STRAND 59 62
SQ SEQUENCE 64 AA; 7038 MW; 05D6454CE7ACD10E CRC64;

Query Match 37.3%; Score 133; DB 1; Length 64;
Best Local Similarity 42.4%; Pred. No. 8.4e-08;
Matches 28; Conservative 12; Mismatches 22; Indels 4; Gaps 2;

QY 1 MRHYLLFALLFLVLPVPG-HGGINTLQKYCRVGRCAVLSCLPKEQIGKSTRG 59
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 1 MRVLYLFSFLFIFLMPPLPGVFGIGDPVT--CLKSGAICHVPFCPRRYKQIGTGLPG 57

QY 60 RKCCR 65
   ||:|:
Db 58 TKCCK 63

RESULT 12
AAH69285 PRELIMINARY; PRT; 64 AA.
AC AAH69285;
DT 01-JUN-2004 (TReMBLrel. 27, Created)
DT 01-JUN-2004 (TReMBLrel. 27, Last sequence update)
DT 01-JUN-2004 (TReMBLrel. 27, Last annotation update)
DE Defensin, beta 4...
GN DEFBA4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

```
OC Mammalia; Eutheria; Primates; Carnivora; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PCR rescued clones;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ueda T.B., Toshlyuk S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=PCR rescued clones;
RA Strausberg R.;
RL Submitted (APR-2004) to the EMBL/Genbank/DBJ databases.
DR EMBL; BC069285; AAH69285.1; -.
SQ SEQUENCE 64 AA; 7038 MW; 05D6454CE7ACD10E CRC64;

Query Match 37.3%; Score 133; DB 2; Length 64;
Best Local Similarity 42.4%; Pred. No. 8.4e-08;
Matches 28; Conservative 12; Mismatches 22; Indels 4; Gaps 2;

QY 1 MRHYLLFALLFLVLPVPG-HGGINTLQKYCRVGRCAVLSCLPKEQIGKSTRG 59
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 1 MRVLYLFSFLFIFLMPPLPGVFGIGDPVT--CLKSGAICHVPFCPRRYKQIGTGLPG 57

QY 60 RKCCR 65
   ||:|:
Db 58 TKCCK 63

RESULT 13
BD03_MOUSE
ID BD03_MOUSE STANDARD; PRT; 63 AA.
AC Q9WTI0;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Beta-defensin 3 precursor (BD-3) (MBD-3).
GN Name=Defb3; Synonyms=Bd3;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.; FUNCTION, INDUCTION, AND TISSUE SPECIFICITY.
RC STRAIN=C57BL/6; TISSUE=Lung;
RX MEDLINE=99307216; PubMed=10377137;
RA Bals R., Wang X., Meegalla R.L., Wattler S., Weiner D.J., Nehls M.C.,
RA Wilson J.M.;
RT "Mouse beta-defensin 3 is an inducible antimicrobial peptide expressed
RT in the epithelia of multiple organs."
RL Infect. Immun. 67:3542-3547 (1999).
RN [2]
RP TISSUE SPECIFICITY.
RC STRAIN=C57BL/6, 129/SvJ, and FVB; TISSUE=Lung;
RX MEDLINE=20517883; PubMed=10922379;
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RA Jia H.P., Mowk S.A., Schutte B.C., Lee S.K., Vivado A., Tack B.F.,
RA Bevins C.L., McCray P.B. Jr.;
RT "A novel murine beta-defensin expressed in tongue, esophagus, and
RT trachea.";
RL J. Biol. Chem. 275:33314-33320(2000).
CC -1- FUNCTION: Antimicrobial activity against Gram-negative bacteria
CC E.coli and P.aeruginosa.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Highest expression in salivary glands,
CC epididymis, ovary and pancreas and to a lesser extent in lung,
CC liver and brain. Low or no expression in skeletal muscle and
CC tongue.
CC -1- INDUCTION: By bacterial infection.
CC -1- SIMILARITY: Belongs to the beta-defensin family. LAP/TAP
CC subfamily.
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CC -----
DR EMBL; AF093245; AAD29573.1; -.
DR EMBL; AF092929; AAD29572.1; -.
DR HSSP; Q15263; 1E4Q.
DR MGD; MGI:1351612; Defb3.
DR InterPro; IPR001855; Defensin_beta.
DR InterPro; IPR006080; Defensin_mammal.
DR Pfam; PF00711; Defensin_beta_1.
DR SMART; SM00048; DEFSN; 1.
DR Antibioc; Cleavage on pair of basic residues; Signal.
KM SIGNAL 1 20 Potential.
FT PROPEP 21 22 Potential.
FT CHAIN 23 63 Beta-defensin 3.
FT DISULFID 31 59 By similarity.
FT DISULFID 38 52 By similarity.
FT DISULFID 42 60 By similarity.
SQ SEQUENCE 63 AA; 7126 MW; 9D59BC8AD16EA330 CRC64;

Query Match 32.6%; Score 116.5; DB 1; Length 63;
Best Local Similarity 43.1%; Pred. No. 7e-06;
Matches 28; Conservative 4; Mismatches 30; Indels 3; Gaps 2;

QY 1 MRIHYLLFALLFLFVVPVPGHGIINTLQKYYCVRVGRCAVLSCLPKEQIGKSTRG 60
Db 1 MRIHYLLFAFLVLLSPAPAFSKIN--NPVSCLRKGRGRC-WNRICGNTRQIGSGVPL 57

QY 61 KCCRR 65
Db 58 KCCRR 62

RESULT 14
EAP_BOVIN
ID EAP_BOVIN STANDARD; PRT; 64 AA.
AC 002775;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Enteric beta-defensin precursor.
GN Name=EBD;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OC NCB1_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98147718; PubMed=9488394;
RA Tarver A.P., Clark D.P., Diamond G., Russell J.P.,
RA Erdjument-Bromage H., Tempst P., Cohen K.S., Jones D.E., Sweeney R.W.,
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RA Wines M., Hwang S., Bevins C.L.;
RT "Enteric beta-defensin: molecular cloning and characterization of a
RT gene with inducible intestinal epithelial cell expression associated
RT with Cryptosporidium parvum infection.";
RL Infect. Immun. 66:1045-1056(1998).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96014297; PubMed=8589529;
RA Gallagher D.S. Jr., Ryan A.M., Diamond G., Bevins C.L., Womack J.E.;
RT "Somatic cell mapping of beta-defensin genes to cattle syntenic group
RT U25 and fluorescence in situ localization to chromosome 27.";
RL Mamm. Genome 6:554-556(1995).
CC -1- FUNCTION: Has antibacterial activity (Potential).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Inducibly expressed in enteric epithelial
CC cells.
CC -1- SIMILARITY: Belongs to the beta-defensin family. LAP/TAP
CC subfamily.
CC -----
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CC -----
DR EMBL; AF000362; AAC48805.1; -.
DR EMBL; AF016539; AAC48804.1; -.
DR HSSP; P46170; 1BNB.
DR InterPro; IPR001855; Defensin_beta.
DR InterPro; IPR006080; Defensin_mammal.
DR Pfam; PF00711; Defensin_beta_1.
DR SMART; SM00048; DEFSN; 1.
DR Antibioc; Signal.
KM SIGNAL 1 26 By similarity.
FT CHAIN 27 64 Enteric beta-defensin.
FT DISULFID 31 60 By similarity.
FT DISULFID 38 53 By similarity.
FT DISULFID 43 61 By similarity.
SQ SEQUENCE 64 AA; 7126 MW; 7E8642AE6F7A6068 CRC64;

Query Match 32.5%; Score 116; DB 1; Length 64;
Best Local Similarity 44.6%; Pred. No. 8.1e-06;
Matches 29; Conservative 4; Mismatches 26; Indels 4; Gaps 2;

QY 1 MRIHYLLFALLFLFVVPVPGH-GGIINTLQKYYCVRVGRCAVLSCLPKEQIGKSTRG 59
Db 1 MRLHLLLTLLFLVLSAGSGFTQGISNPLS---CRUNRGICVPIRCPSGNLRQIGTCFTPS 57

QY 60 RKCCR 64
Db 58 VKCCR 62

RESULT 15
Q71UAS
ID Q71UAS PRELIMINARY; PRT; 60 AA.
AC Q71UAS;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Neutrophil beta-defensin 12 (Fragment).
GN Name=NBD12;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OC NCB1_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99403068; PubMed=10473579;
RA Yount N.Y., Yuan J., Tarver A., Castro T., Diamond G., Tran P.A.,
```



RA Levy J.N., McCullough C., Cullor J.S., Bevins C.L., Selsted M.E.;  
RT "Cloning and expression of bovine neutrophil beta-defensins.  
RT Biosynthetic profile during neutrophilic maturation and localization  
RT of mature peptide to novel cytoplasmic dense granules.";  
RL J. Biol. Chem. 274:26249-26258(1999).  
DR EMBL; AF105370; AAD43032.1; JOINED.  
DR EMBL; AF105371; AAD43032.1; -.  
DR InterPro; IPR001855; Defensin\_beta.  
DR InterPro; IPR006080; Defensin\_mammal.  
DR Pfam; PF00711; Defensin\_beta; 1.  
DR SMART; SM00048; DEFSN; 1.  
FT NON TER 60  
SQ SEQUENCE 60 AA; 6464 MW; 38668779EACF66DE CRC64;

Query Match 32.2%; Score 115; DB 2; Length 60;  
Best Local Similarity 42.2%; Pred. No. 1e-05;  
Matches 27; Conservative 5; Mismatches 26; Indels 6; Gaps 1;

QY 1 MRLHYLLFAULFLFVVPVPGHGIIINTLQKYCYCRVRGRCAYLSCLPKEDQIGKSTRGR 60  
DB 1 MRLHYLLALLFLVLSAASGISGPLS-----CGRNGVCIPIRCPVPMRQIGTCFGRPV 54

QY 61 KCCR 64  
DB 55 KCCR 58

Search completed: October 13, 2004, 14:50:38  
Job time : 200 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 13, 2004, 14:42:12 ; Search time 39 Seconds  
(without alignments)  
160.361 Million cell updates/sec

Title: US-10-272-121-2  
Perfect score: 357  
Sequence: 1 MRHYLLFALLFLVLPVPG.....LPKEQIGKSTRGRKCCR 65  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_79:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	108	30.3	64	2 A56128	lingual antimicrob
2	108	30.3	65	2 A35947	crotonamine 1 precu
3	108	30.3	65	2 C35947	crotonamine 3 precu
4	106	29.7	64	2 A47438	airway epithelial
5	103	28.9	65	2 JC5324	myotoxin a precurs
6	89	24.9	42	2 F45495	beta-defensin-6 -
7	83	23.2	64	2 B35947	crotonamine 2 precu
8	75	21.0	38	2 B47753	beta-defensin-11 -
9	71	19.9	42	2 C45495	beta-defensin-3 -
10	69.5	19.5	45	2 A37909	myotoxin - eastern
11	69.5	19.5	95	1 WTRBM1	macrophage antibio
12	69	19.3	40	2 G45495	beta-defensin-7 -
13	69	19.3	40	2 I45495	beta-defensin-9 -
14	68	19.0	42	2 D47753	beta-defensin-13 -
15	66.5	18.6	43	1 CXRSCH	toxic peptide C -
16	65.5	18.3	42	1 CXRSMT	crotonamine - tropic
17	65.5	18.3	95	1 WTRBM2	defensin CS-4 prec
18	63.5	17.8	51	2 D35947	crotonamine 4 precu
19	62.5	17.5	42	1 MXRSMV	myotoxin a 6 - pra
20	61	17.1	122	2 JC6548	high sulfur protei
21	61	17.1	218	2 T22261	hypothetical prote
22	61	17.1	524	2 S38539	disintegrin-like m
23	61	17.1	670	2 I65967	disintegrin-like m
24	60.5	16.9	40	2 C39560	myotoxin a 5 - pra
25	60	16.8	32	2 E59076	defensin alpha-5 -
26	60	16.8	32	2 G59076	defensin alpha-7 -
27	60	16.8	33	2 D59076	defensin alpha-4 -
28	60	16.8	33	2 F59076	defensin alpha-6 -
29	60	16.8	855	2 T05981	hypothetical prote

30	59.5	16.7	260	2 AD2461	hypothetical prote
31	59.5	16.7	454	2 B82412	probable magnesium
32	59.5	16.7	1184	2 T09484	cartilage intermed
33	59	16.5	40	2 E45495	beta-defensin-5 -
34	59	16.5	177	2 S37650	high-sulfur kerati
35	59	16.5	263	2 S57346	interleukin 15 rec
36	58.5	16.4	43	2 A29089	myotoxin I - midge
37	58.5	16.4	45	2 S12909	myotoxin - western
38	58.5	16.4	88	2 H69475	hypothetical prote
39	58.5	16.4	112	2 A46717	colipase precursor
40	58.5	16.4	359	2 A96816	P9K20.25 (imported
41	58	16.2	34	2 C49195	corticostatic pept
42	58	16.2	152	2 I47109	high-sulfur wool m
43	58	16.2	152	2 I47112	high-sulfur wool m
44	58	16.2	162	2 I47107	high-sulfur wool m
45	58	16.2	172	1 KRSHHA	keratin high-sulfu

ALIGNMENTS

RESULT 1  
A56128  
lingual antimicrobial peptide precursor - bovine  
C/Species: Bos primigenius taurus (cattle)  
C/Date: 05-Jan-1996 #sequence\_revision 05-Jan-1996 #text\_change 09-Jul-2004  
R/Schönwetter, B.S.; Stolzenberg, E.D.; Zasloff, M.A.  
Science 267, 1645-1648, 1995  
A/Title: Epithelial antibiotics induced at sites of inflammation.  
A/Reference number: A56128; MUID:95192714; PMID:7886453  
A/Accession: A56128  
A/Molecule type: mRNA  
A/Residues: 1-64 <SCH>  
A/Cross-references: UNIPROT:Q28880; GB:S76279; NID:9894208; PIDN:AAB33727.1; PID:989420  
A/Accession: B56128  
A/Molecule type: protein  
A/Residues: 23-64 <SC2>  
C/Keywords: antibacterial; antifungal  
F/1-20/Domain: signal sequence #status predicted <SIG>  
F/23-64/Product: lingual antimicrobial peptide #status experimental <MAT>

Query Match 30.3%; Score 108; DB 2; Length 64;  
Best Local Similarity 41.5%; Pred. No. 1.7e-05;  
Matches 27; Conservative 3; Mismatches 33; Indels 2; Gaps 1;

QY 1 MRHYLLFALLFLVLPVPGHGIIINTQKYCRVRGRCVAVSLPKEQIGKSTRGR 60  
DB 1 MRHYLLFALLFLVLPVPGHGIIINTQKYCRVRGRCVAVSLPKEQIGKSTRGR 60  
QY 61 KCCR 65  
DB 59 KCCR 63

RESULT 2  
A35947  
crotonamine 1 precursor - tropical rattlesnake  
C/Species: Crotalus durissus terrificus (tropical rattlesnake, cascabel)  
C/Date: 14-Dec-1990 #sequence\_revision 14-Dec-1990 #text\_change 09-Jul-2004  
R/Smith, L.A.; Schmidt, J.J.  
Toxicon 28, 575-585, 1990  
A/Title: Cloning and nucleotide sequences of crotonamine genes.  
A/Reference number: A35947; MUID:90357261; PMID:2389256  
A/Accession: A35947  
A/Status: preliminary; not compared with conceptual translation  
A/Molecule type: mRNA  
A/Residues: 1-65 <SMI>  
A/Cross-references: UNIPROT:P24331  
C/Superfamily: crotonamine

Query Match 30.3%; Score 108; DB 2; Length 65;

Best Local Similarity 39.1%; Pred. No. 1.8e-05;  
Matches 27; Conservative 9; Mismatches 21; Indels 12; Gaps 5;

### RESULT 3

croctamine 3 precursor - tropical rattlesnake  
 C/Species: Crotalus durissus terrificus (tropical rattlesnake,  
 C/Date: 14-Dec-1990 #sequence\_revision 14-Dec-1990 #text\_change  
 C/Accession: C35947  
 R/Smith, J.A.; Schmidt, J.J.  
 Toxicon 28, 575-585, 1990  
 A/Title: Cloning and nucleotide sequences of croctamine genes.  
 A/Reference number: A35947; MUID:90357261; PMID:2389256  
 A/Accession: C35947  
 A/Status: preliminary; not compared with conceptual translation  
 A/Molecule type: mRNA  
 A/Residues: 1-65 <SMT>  
 A/Cross-references: UNIPROT:P24333  
 C/Superfamily: croctamine

Query Match	30.3%;	Score 108;	DB 2;	Length 65;
Best Local Similarity	39.1%;	Pred. No. 1.8e-05;		
Matches 27;	Conservative	9;	Mismatches 21;	Indels 12;
				Gaps 5;

[illegible]

## RESULT 4

airway epithelial antimicrobial peptide TAP precursor - bovine  
N;Alternate names: antimicrobial peptide, tracheal  
C/Species: Bos primigenius taurus (cattle)  
C/Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 09-Jul-2004  
C/Accession: A47438; A39397  
R;Diamond, G.; Jones, D.E.; Bevins, C.L.  
Proc. Natl. Acad. Sci. U.S.A. 90, 4596-4600, 1993  
A;Title: Airway epithelial cells are the site of expression of a mammalian antimicrobial  
A;Reference number: A47438; MUID:93281626; PMID:8506305  
A;Accession: A47438  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-64 <DIA>  
A;Cross-references: UNIPROT:P25068; GB:L13373; NID:G289395; PIDN:AAA72363.1; PID:G289396  
R;Diamond, G.; Zasloff, M.; Eck, H.; Brasseur, M.; Maloy, W.L.; Bevins, C.L.  
Proc. Natl. Acad. Sci. U.S.A. 88, 3952-3956, 1991  
A;Title: Tracheal antimicrobial peptide, a cysteine-rich peptide from mammalian tracheal  
A;Reference number: A39397; MUID:91219490; PMID:2023943  
A;Accession: A39397  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-64 <DI2>  
A;Cross-references: GB:M63023; NID:G2226433; PIDN:AAB61757.1; PID:G163740  
C;Genetics:  
A;Introns: 19/2  
F;1-26/Domain: signal sequence #status predicted <SIG>  
F;27-64/Product: airway epithelial antimicrobial peptide TAP #status predicted <MAT>

Query Match 29.7%; Score 106; DB 2; Length 64;

Best Local Similarity	40.9%;	Pred. No. 2.9e-05;
Matches	27;	Conservative 7; Mismatches 28; Indels 4; Gaps 2;

QY 1 MRIHYLLFALLLEFLVPPVPGH-GGIINTLQKYYCRVRGGRCVAVLSCLPKEQIQKSTRG 59  
||:|:| | | | | | : | : | | | | |  
Db 1 MRUHLHLLALLFLVLSAMSGFTQGVGNFVS---CVRNKGICVPIRCPSGSMKQIGTCVGRA 57

QY	60	RKCCRR	65
		:	
Db	58	VKCCRK	63

## RESULT 5

myotoxin a precursor - prairie rattlesnake  
 C/Species: Crotalus viridis viridis (prairie rattlesnake)  
 C/Date: 15-May-1997 #sequence\_revision 18-Jul-1997 #text\_change 02-Jul-1998  
 C/Accession: J05324  
 R/Norris, J.W.; Fry, R.M.; Tu, A.T.  
 Biochem. Biophys. Res. Commun. 230, 607-610, 1997  
 A/Title: The nucleotide sequence of the translated and untranslated regions of a cDNA f  
 A/Reference number: J05324; NUID:97167753; PMID:9015371  
 A/Accession: J05324  
 A/Molecule type: mRNA  
 A/Residues: 1-65 <NOR>  
 A/Experimental source: venom  
 A/Note: the authors translated the codon CAG for residue 27 as His and CTT for residue  
 C/Comment: This protein inhibits Ca2+ uptake into the sarcoplasmic reticulum by binding  
 C/Superfamily: crotamine  
 F;1-22/Domain: signal sequence #status predicted <SIG>  
 F;23-64/Product: myotoxin a #status predicted <Mat>

Query Match	28.5%;	Score 103;	DB 2;	Length 65;
Best Local Similarity	36.8%;	Pred. No. 6.6e-05;		
Matches 25;	Conservative 11;	Mismatches 22;	Indels 10;	Gaps 4;

```
QY 1 MEIHYLLFALLFLFVLVPVPGHGIINTLQKYCYVVGRCAYLS--CLPKKEQIGKSTR 58
      |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 1 MKILYLLFAFLFLFAFLSEPG-----NAYKQ--CQKKGGHCFPKEKICIPSSDLGKMDCR 53
      |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 59 GR-KCCRR 65
      :|::|::|
Db 54 WKMKCCCK 61
```

## RESULT 6

beta-defensin-6 - bovine  
N/Alternate names: peptidase BNBD-6  
C/Species: Bos primigenius taurus (cattle)  
C/Date: 24-Feb-1994 #sequence\_revision 22-Apr-1995 #text\_change 09-Jul-2004  
C/Accession: F45495  
R:Selsted, M.E.; Tang, Y.Q.; Morris, W.L.; McGuire, P.A.; Novotny, M.J.; Smith, W.; Hen-  
J. Biol. Chem. 268, 6641-6648, 1993  
A/Title: Purification, primary structures, and antibacterial activities of beta-defensi-  
A/Reference number: A45495; MUID:93203264; PMID:8454635  
A/Accession: F45495  
A/Molecule type: protein  
A/Residues: 1-42 <SEL>  
A/Cross-references: UNIPROT:P46164  
A/Note: sequence modified after extraction from NCBI backbone  
C/Keywords: antibacterial; disulfide bond; pyroglutamic acid  
F:1-42/Product: beta-defensin-6 #status experimental <Mal>  
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F:9-38,16-31,21-39/Disulfide bonds: #status predicted

Query Match	24.9%	Score 89;	DB 2;	Length 42;
Best Local Similarity	48.5%	Pred. No. 0.0019;		
Matches 16;	Conservative 3;	Mismatches 14;	Indels 0;	Gaps 0;

```

QY      33 CRVGGRCVAVLSCLPEKEQIGKSTGRKCCR 65
      ||: ||| : | : ||| | ||||
Db      9 CRVGGFCVPIRCPGRTRQIGTCFGRPVKCCR 41

```



## RESULT 7

B35947  
crotamine 2 precursor - tropical rattlesnake (fragment)  
C/Species: Crotalus durissus terrificus (tropical rattlesnake, cascabel)  
C/Date: 14-Dec-1990 #sequence\_revision 14-Dec-1990 #text\_change 09-Jul-2004  
C/Accession: B35947  
R/Smith, L.A.; Schmidt, J.J.  
Toxicon 28, 575-585, 1990  
A/Title: Cloning and nucleotide sequences of crotamine genes.  
A/Reference number: A35947; MUID:90357261; PMID:2389256  
A/Accession: B35947  
A/Status: preliminary; not compared with conceptual translation  
A/Molecule type: mRNA  
A/Residues: 1-64 <SMI>  
A/Cross-references: UNIPROT:P24332  
C/Superfamily: crotamine

Query Match 23.2%; Score 83; DB 2; Length 64;  
Best Local Similarity 35.3%; Pred. No. 0.013;  
Matches 24; Conservative 9; Mismatches 23; Indels 12; Gaps 5;

QY 2 RIHYLLFALLFLVFPVPGHGINTLQKYRCVRGRCVLS--CLPKKEQIGK--CST 57

Db 1 KIILYLLFAFLFLAFLSEPG-----NAYKR--CHIKGHCFPKEKICIPSSDFGKMDCPW 53

QY 58 RGRKCCRR 65

Db 54 R-RKSLKK 60

## RESULT 8

B47753  
beta-defensin-11 - bovine  
N/Alternate names: peptide BNBD-11  
C/Species: Bos primigenius taurus (cattle)  
C/Date: 24-Feb-1994 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004  
C/Accession: B47753  
R/Selsted, M.E.; Tang, Y.Q.; Morris, W.L.; McGuire, P.A.; Novotny, M.J.; Smith, W.; Hens  
J. Biol. Chem. 268, 6641-6648, 1993  
A/Title: Purification, primary structures, and antibacterial activities of beta-defensin  
A/Reference number: A45495; MUID:93203264; PMID:8454635  
A/Accession: B47753  
A/Molecule type: protein  
A/Residues: 1-38 <SEL>  
A/Cross-references: UNIPROT:P46169  
A/Note: sequence extracted from NCBI backbone (NCBIP:127961)  
C/Keywords: antibacterial; disulfide bond  
F/1-38/Product: beta-defensin-11 #status experimental <MA1>  
F/5-34,12-27,17-35/Disulfide bonds: #status predicted

Query Match 21.0%; Score 75; DB 2; Length 38;  
Best Local Similarity 46.9%; Pred. No. 0.072;  
Matches 15; Conservative 1; Mismatches 16; Indels 0; Gaps 0;

QY 33 CRVRGRCVLSCLPKKEQIGKSTRGRKCCR 64

Db 5 CRRNGVCIPRCRCPGRMQIGTCFGRPVKCCR 36

## RESULT 9

C45495  
beta-defensin-3 - bovine  
N/Alternate names: peptide BNBD-3  
N/Contains: beta-defensin-2  
C/Species: Bos primigenius taurus (cattle)  
C/Date: 24-Feb-1994 #sequence\_revision 22-Apr-1995 #text\_change 09-Jul-2004  
C/Accession: C45495; B45495  
R/Selsted, M.E.; Tang, Y.Q.; Morris, W.L.; McGuire, P.A.; Novotny, M.J.; Smith, W.; Hens  
J. Biol. Chem. 268, 6641-6648, 1993  
A/Title: Purification, primary structures, and antibacterial activities of beta-defensin  
A/Reference number: A45495; MUID:93203264; PMID:8454635

A/Accession: C45495  
A/Molecule type: protein  
A/Residues: 1-42 <SEL>

A/Cross-references: UNIPROT:P46160  
A/Note: sequence modified after extraction from NCBI backbone  
A/Accession: B45495  
A/Molecule type: protein  
A/Residues: 3-42 <SE2>  
A/Note: sequence extracted from NCBI backbone (NCBIP:127952)  
C/Keywords: antibacterial; disulfide bond; pyroglutamic acid  
F/1-42/Product: beta-defensin-3 #status experimental <MA1>  
F/3-42/Product: beta-defensin-2 #status experimental <MA2>  
F/1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F/9-38,16-31,21-39/Disulfide bonds: #status predicted

Query Match 19.9%; Score 71; DB 2; Length 42;  
Best Local Similarity 40.6%; Pred. No. 0.22;  
Matches 13; Conservative 3; Mismatches 16; Indels 0; Gaps 0;

QY 33 CRVRGRCVLSCLPKKEQIGKSTRGRKCCR 64

Db 9 CRINRGFCVPICRCPGRTRQIGTCFGRPIKCCR 40

## RESULT 10

A37909  
myotoxin - eastern diamondback rattlesnake  
C/Species: Crotalus adamanteus (eastern diamondback rattlesnake)  
C/Date: 31-Jan-1992 #sequence\_revision 31-Jan-1992 #text\_change 09-Jul-2004  
C/Accession: A37909  
R/Samejima, Y.; Ackl, Y.; Mebs, D.  
Toxicon 29, 461-468, 1991  
A/Title: Amino acid sequence of a myotoxin from venom of the eastern diamondback rattles  
A/Reference number: A37909; MUID:91320359; PMID:1862521  
A/Accession: A37909  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-45 <SAM>  
A/Cross-references: UNIPROT:P24330  
C/Superfamily: crotoamine  
C/Keywords: myotoxin

Query Match 19.5%; Score 69.5; DB 2; Length 45;  
Best Local Similarity 38.9%; Pred. No. 0.35;  
Matches 14; Conservative 4; Mismatches 15; Indels 3; Gaps 2;

QY 33 CRVRGRC--AVLSCLPKKEQIGKSTRGR-KCCRR 65

Db 4 CHKKGGHCFPKTVICLPSSDFGKMDCRWRWKCKCK 39

## RESULT 11

WTRBML  
macrophage antibiotic peptide MCP-1 - rabbit  
N/Alternate names: antiadrenocorticotropin, corticostatic peptide CS-3; defensin  
C/Species: Oryctolagus cuniculus (domestic rabbit)  
C/Date: 28-Aug-1985 #sequence\_revision 23-Feb-1996 #text\_change 09-Jul-2004  
C/Accession: A45811; A01647; A22569; B49195  
R/Ganz, T.; Rayner, J.R.; Valore, E.V.; Tumolo, A.; Talmadge, K.; Fuller, F.  
J. Immunol. 143, 1358-1365, 1989  
A/Title: The structure of the rabbit macrophage defensin genes and their organ-specific  
A/Reference number: A45811; MUID:89309825; PMID:2745983  
A/Accession: A45811  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-95 <GAN>  
A/Cross-references: UNIPROT:P01376; GB:M28072; NID:9165473; PIDN:AAA31388.1; PID:9165474  
R/Selsted, M.E.; Brown, D.M.; Delange, R.J.; Lehrer, R.I.  
J. Biol. Chem. 258, 14485-14489, 1983  
A/Title: Primary structures of MCP-1 and MCP-2, natural peptide antibiotics of rabbit lu  
A/Reference number: A01647; MUID:84061901; PMID:6643497  
A/Accession: A01647  
A/Molecule type: protein

A/Residues: 63-95 <SE1>  
R/Selected: M.E.; Brown, D.M.; Delange, R.J.; Harwig, S.S.L.; Lehrer, R.I.  
J. Biol. Chem. 260, 4579-4584, 1985  
A/Title: Primary structures of six antimicrobial peptides of rabbit peritoneal neutrophils  
A/Reference number: A22569; MUID:85182561; PMID:3988726  
A/Accession: A22569  
A/Molecule type: protein  
A/Residues: 63-95 <SE2>  
A/Experimental source: peritoneal neutrophils  
R/Zhu, Q.; Solomon, S.  
Endocrinology 130, 1413-1423, 1992  
A/Title: Isolation and mode of action of rabbit corticostatic (antiadrenocorticotropin)  
A/Reference number: A49195; MUID:92164536; PMID:1311240  
A/Accession: B49195  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 63-95 <ZHU>  
A/Note: sequence extracted from NCBI backbone (NCBIF:85970)  
C/Comment: This peptide is active against some fungi and gram-positive bacteria in vitro  
C/Superfamily: mammalian defensin  
C/Keywords: antibacterial  
F;65-93, 67-82, 72-92/Disulfide bonds: #status predicted

Query Match	19.5%;	Score 69.5;	DB 1;	Length 95;
Best Local Similarity	48.3%;	Pred. No. 0.65;		
Matches	14;	Conservative	2;	Mismatches 10;
				Indels 3;
				Gaps 1;

```

QY      40 CAVLSCLPKEEQIGKSTTGR---KCCR 65
      ||| : | | | | |
Db      67 CRALCLPRERAGFCRTGRHPLCCR 95

```

RESULT 12  
G45495

beta-defensin-7 - bovine  
N;Alternate names: peptidase BNBD-7  
C;Species: Bos primigenius taurus (cattle)  
C;Date: 24-Feb-1994 #sequence\_revision 22-Apr-1995 #text\_change 09-Jul-2004  
C;Accession: G45495  
R;Selsited, M.E.; Tang, Y.Q.; Morris, W.L.; McGuire, P.A.; Novotny, M.J.; Smith, W.; Hens  
J. Biol. Chem. 268, 6641-6648, 1993  
A;Title: Purification, primary structures, and antibacterial activities of beta-defensin  
A;Reference number: A45495; MUID:93203264; PMID:8454635  
A;Accession: G45495  
A;Molecule type: protein  
A;Residues: 1-40 <SEL>  
A;Cross-references: UNIPROT:P46165  
A;Note: sequence modified after extraction from NCBI backbone  
C;Keywords: antibacterial; disulfide bond; pyroglutamic acid  
F;1-40/Product: beta-defensin-7 #status experimental <Val>  
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F;9-38,16-31,21-39/Disulfide bonds: #status predicted

Query Match	19.3%;	Score 69;	DB 2;	Length 40;
Best Local Similarity	40.6%;	Pred. No. 0.37;		
Matches 13; Conservative	2;	Mismatches 17;	Indels 0;	Gaps 0;

QY 33 CRVRGRCVLSCLPKKEQIGKCTRGRCCR 64  
|| : | : ||| |  
DB 9 CRINRGCVPIRCPGHRROIGTCLGPRIKCR 40

## RESULT 13

I45495  
beta-defensin-9 - bovine  
N;Alternate names: peptide BNBD-9  
N;Contains: beta-defensin-8  
C;Species: Bos primigenius taurus (cattle)  
C;Date: 24-Feb-1994 #sequence\_revision 22-Apr-1995 #text\_change 09-Jul-2004  
C;Accession: I45495; H45495  
R;Seasted, M.E.; Tang, Y.Q.; Morris, W.L.; McGuire, P.A.; Novotny, M.J.; Smith, W.; Hens  
J. Biol. Chem. 268, 6641-6648, 1993  
A;Title: Purification, primary structures, and antibacterial activities of beta-defensin

```

A;Reference number: A45495; MUID:93203264; PMID:8454635
A;Accession: I45495
A;Molecule type: protein
A;Residues: 1-40 <SEL>
A;Cross-references: UNIPROT:P46166
A;Note: sequence modified after extraction from NCBI backbone
A;Accession: H45495
A;Molecule type: protein
A;Residues: 3-40 <SEL>
A;Note: sequence extracted from NCBI backbone (NCBIF:127958)
C;Keywords: pyroglutamic acid
F;1-40/Product: beta-defensin-9 #status experimental <MA1>
F;3-40/Product: beta-defensin-8 #status experimental <MA2>
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;9-38,16-31,21-39/Disulfide bonds: #status predicted

Query Match      19.3%; Score 69; DB 2; Length 40;
Best Local Similarity 40.6%; Pred. No. 0.37;
Matches 13; Conservative 2; Mismatches 17; Indels 0; Gaps 0;

```

QY 33 CRVGRCAVLSCLPKEQIGKSTGRGCCR 64  
||: ||| : ||| ||| ||| ||| |||

Db 9 CRINGECVPTRCPGHRQIGTCLGPQIKCR 40

RESULT 14  
D47753

beta-defensin-13 - bovine  
N/Alternate names: peptide BNB-13  
N/Contains: beta-defensin-12  
C/Species: Bos primigenius taurus (cattle)  
C/Date: 24-Feb-1994 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004  
C/Accession: D47753; C47753  
R/Selsted, M.E.; Tang, Y.Q.; Morris, W.L.; McGuire, P.A.; Novotny, M.J.; Smith, W.; Hen-  
J. Biol. Chem. 268, 6641-6648, 1993  
A/Title: Purification, primary structures, and antibacterial activities of beta-defensin  
A/Reference number: A45495; MUID:93203264; PMID:8454635  
A/Accession: D47753  
A:Molecule type: protein  
A:Residues: 1-42 <SEL>  
A/Cross-references: UNIPROT:P46171  
A/Note: sequence extracted from NCBI backbone (NCBIP:127963)  
A/Accession: C47753  
A:Molecule type: protein  
A:Residues: 5-42 <SE2>  
A/Note: sequence extracted from NCBI backbone (NCBIP:127962)  
C/Keywords: disulfide bond  
F/1-42/Product: beta-defensin-13 #status experimental <MA1>  
F/5-42/Product: beta-defensin-12 #status experimental <MA2>  
F/9-38,16-31,21-39/Disulfide bonds: #status experimental

Query Match	19.0%;	Score 68;	DB 2;	Length 42;
Best Local Similarity	43.8%;	Pred. No. 0.5;		
Matches 14; Conservative	1;	Mismatches 17;	Indels 0;	Gaps 0;

QY 33 CRVRGERCAVLSCLPKEEQIGKCSSTRGRKCCR 64  
| | | : | | | | |  
Db 9 CGRNGVCTPIRCVPVMRQIGTCFGRPVKCCR 40

## RESULT 15

C/Species: *Crotalus viridis helleri* (southern Pacific rattlesnake)  
 C/Date: 31-May-1979 #sequence\_revision 08-Oct-1981 #text\_change 09-Jul-2004  
 C/Accession: A01737  
 R/Maeda, N.; Tamiya, N.; Pattabhiraman, T.R.; Russell, F.E.  
 Toxicon 16, 431-441, 1978  
 A/Title: Some chemical properties of the venom of the rattlesnake, *Crotalus viridis helleri*  
 A/Reference number: A01737; MUID:79015339; PMID:694946  
 A/Accession: A01737  
 A/Molecule type: protein  
 A/Residues: 1-43 <MAE>

A;Cross-references: UNIPROT:P01477  
C;Superfamily: croctamine  
C;Keywords: myotoxin; venom  
F;4-36,11-30,18-37/Disulfide bonds: #status predicted

Query Match	18.6%	Score 66.5;	DB 1;	Length 43;
Best Local Similarity	36.1%;	Pred. No. 0.76;		
Matches	13;	Mismatches	15;	Indels 3;
				Gaps 2;

QY 33 CRVRGRC--AVLSCLPKKEOIGKCGSTRGR-KCCR 65  
| : ||| | : ||| :  
4 CHKKGSHFPKTVICLPSSDFGKMDCRWKWKCKK 39  
DB

Search completed: October 13, 2004, 14:51:17  
Job time : 40 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 13, 2004, 14:44:44 ; Search time 131 Seconds  
(without alignments)  
160.110 Million cell updates/sec

Title: US-10-272-121-2  
Perfect score: 357  
Sequence: 1 MRIHYLLFALLFLVVPVPG.....LPKEDQIGKSTRGRKCCR 65

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1356558 seqs, 322682953 residues

Total number of hits satisfying chosen parameters: 1356558

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*  
2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep:\*  
3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*  
4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep:\*  
5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep:\*  
6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep:\*  
7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep:\*  
8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*  
9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep:\*  
10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep:\*  
11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep:\*  
12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep:\*  
13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep:\*  
14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep:\*  
15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep:\*  
16: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pep:\*  
17: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep:\*  
18: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\*  
19: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	357	100.0	65	14	US-10-091-166B-2 Sequence 2, Appli
2	357	100.0	65	14	US-10-272-121-2 Sequence 2, Appli
3	357	100.0	65	14	US-10-409-366-2 Sequence 2, Appli
4	357	100.0	65	14	US-10-409-532-2 Sequence 2, Appli
5	357	100.0	67	9	US-09-917-340-52 Sequence 52, Appli
6	357	100.0	67	9	US-09-917-340-72 Sequence 72, Appli
7	357	100.0	67	9	US-09-872-852-2 Sequence 2, Appli
8	357	100.0	67	14	US-10-091-166B-10 Sequence 10, Appli
9	357	100.0	67	14	US-10-272-121-10 Sequence 10, Appli
10	357	100.0	67	14	US-10-409-366-10 Sequence 10, Appli
11	357	100.0	67	14	US-10-409-532-10 Sequence 10, Appli
12	240	67.2	45	9	US-09-872-852-4 Sequence 4, Appli
13	234	65.5	44	16	US-10-332-765-27 Sequence 27, Appli
14	231	64.7	48	14	US-10-091-166B-36 Sequence 36, Appli

15	231	64.7	48	14	US-10-272-121-36	Sequence 36, Appli
16	231	64.7	48	14	US-10-409-366-36	Sequence 36, Appli
17	231	64.7	48	14	US-10-409-532-36	Sequence 36, Appli
18	231	64.7	49	14	US-10-091-166B-35	Sequence 35, Appli
19	231	64.7	49	14	US-10-272-121-35	Sequence 35, Appli
20	231	64.7	49	14	US-10-409-366-35	Sequence 35, Appli
21	231	64.7	49	14	US-10-409-532-35	Sequence 35, Appli
22	224	62.7	47	14	US-10-091-166B-38	Sequence 38, Appli
23	224	62.7	47	14	US-10-272-121-38	Sequence 38, Appli
24	224	62.7	47	14	US-10-409-366-38	Sequence 38, Appli
25	224	62.7	47	14	US-10-409-532-38	Sequence 38, Appli
26	224	62.7	48	14	US-10-091-166B-37	Sequence 37, Appli
27	224	62.7	48	14	US-10-272-121-37	Sequence 37, Appli
28	224	62.7	48	14	US-10-409-366-37	Sequence 37, Appli
29	224	62.7	48	14	US-10-409-532-37	Sequence 37, Appli
30	220	61.6	41	9	US-09-872-852-3	Sequence 3, Appli
31	218	61.1	46	14	US-10-091-166B-40	Sequence 40, Appli
32	218	61.1	46	14	US-10-272-121-40	Sequence 40, Appli
33	218	61.1	46	14	US-10-409-366-40	Sequence 40, Appli
34	218	61.1	46	14	US-10-409-532-40	Sequence 40, Appli
35	218	61.1	47	14	US-10-091-166B-39	Sequence 39, Appli
36	218	61.1	47	14	US-10-272-121-39	Sequence 39, Appli
37	218	61.1	47	14	US-10-409-366-39	Sequence 39, Appli
38	218	61.1	47	14	US-10-409-532-39	Sequence 39, Appli
39	210	58.8	45	14	US-10-091-166B-42	Sequence 42, Appli
40	210	58.8	45	14	US-10-272-121-42	Sequence 42, Appli
41	210	58.8	45	14	US-10-409-366-42	Sequence 42, Appli
42	210	58.8	45	14	US-10-409-532-42	Sequence 42, Appli
43	210	58.8	46	14	US-10-091-166B-41	Sequence 41, Appli
44	210	58.8	46	14	US-10-272-121-41	Sequence 41, Appli
45	210	58.8	46	14	US-10-409-366-41	Sequence 41, Appli

ALIGNMENTS

RESULT 1  
US-10-091-166B-2  
; Sequence 2, Application US/10091166B  
; Publication No. US20030143671A1  
; GENERAL INFORMATION:  
; APPLICANT: Adler, David A.  
; APPLICANT: Holloway, James L.  
; APPLICANT: Baidur, Nand  
; APPLICANT: Belgel-Orme, Stephanie  
; APPLICANT: Shepard, Paul O.  
; TITLE OF INVENTION: NOVEL BETA-DEFENSINS  
; FILE REFERENCE: 97-44D1  
; CURRENT APPLICATION NUMBER: US/10/091,166B  
; PRIOR FILING DATE: 2002-03-05  
; PRIOR APPLICATION NUMBER: US 09/636,399  
; PRIOR FILING DATE: 2000-08-10  
; PRIOR APPLICATION NUMBER: US 09/344,097  
; PRIOR FILING DATE: 1999-06-25  
; PRIOR APPLICATION NUMBER: US 09/150,786  
; PRIOR FILING DATE: 1998-09-10  
; PRIOR APPLICATION NUMBER: US 60/064,294  
; PRIOR FILING DATE: 1997-11-05  
; PRIOR APPLICATION NUMBER: US 60/058,335  
; PRIOR FILING DATE: 1997-09-10  
; NUMBER OF SEQ ID NOS: 72  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 65  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-10-091-166B-2

Query Match 100.0%; Score 357; DB 14; Length 65;  
Best Local Similarity 100.0%; Pred. No. 3.2e-35;  
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRIHYLLFALLFLVVPVPGHGINTLQKYYCVRGRCAYLSCLPKEDQIGKSTRGR 60

Db 1 MRIHYLLFALLFLVLPVPGHGIINTLQKYCRVRGRCAYLSCLPKKEQIGKCTRGR 60

QY 61 KCCRR 65  
Db 61 KCCRR 65

## RESULT 2

US-10-272-121-2  
; Sequence 2, Application US/10272121  
; Publication No. US20030157638A1  
; GENERAL INFORMATION:  
; APPLICANT: Adler, David A.  
; APPLICANT: Holloway, James L.  
; APPLICANT: Baidur, Nand  
; APPLICANT: Beigel-Orme, Stephanie  
; APPLICANT: Sheppard, Paul O.  
; TITLE OF INVENTION: NOVEL BETA-DEFENSINS  
; FILE REFERENCE: 97-44D2  
; CURRENT APPLICATION NUMBER: US/10/272,121  
; CURRENT FILING DATE: 2002-10-15  
; PRIOR APPLICATION NUMBER: US 09/636,399  
; PRIOR FILING DATE: 2000-08-10  
; PRIOR APPLICATION NUMBER: US 09/344,097  
; PRIOR FILING DATE: 1999-06-25  
; PRIOR APPLICATION NUMBER: US 09/150,786  
; PRIOR FILING DATE: 1998-09-10  
; PRIOR APPLICATION NUMBER: US 60/064,294  
; PRIOR FILING DATE: 1997-11-05  
; PRIOR APPLICATION NUMBER: US 60/058,335  
; PRIOR FILING DATE: 1997-09-10  
; NUMBER OF SEQ ID NOS: 72  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 65  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-272-121-2

Query Match 100.0%; Score 357; DB 14; Length 65;  
Best Local Similarity 100.0%; Pred. No. 3.2e-35;  
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRIHYLLFALLFLVLPVPGHGIINTLQKYCRVRGRCAYLSCLPKKEQIGKCTRGR 60  
Db 1 MRIHYLLFALLFLVLPVPGHGIINTLQKYCRVRGRCAYLSCLPKKEQIGKCTRGR 60

QY 61 KCCRR 65  
Db 61 KCCRR 65

## RESULT 3

US-10-409-366-2  
; Sequence 2, Application US/10409366  
; Publication No. US20030166912A1  
; GENERAL INFORMATION:  
; APPLICANT: Adler, David A.  
; APPLICANT: Holloway, James L.  
; APPLICANT: Baidur, Nand  
; APPLICANT: Beigel-Orme, Stephanie  
; APPLICANT: Sheppard, Paul O.  
; TITLE OF INVENTION: NOVEL BETA-DEFENSINS  
; FILE REFERENCE: 97-44C2  
; CURRENT APPLICATION NUMBER: US/10/409,366  
; CURRENT FILING DATE: 2003-04-07  
; PRIOR APPLICATION NUMBER: US/09/636,399A  
; PRIOR FILING DATE: 2000-08-10  
; PRIOR APPLICATION NUMBER: 60/058,335  
; PRIOR FILING DATE: 1997-10-09  
; PRIOR APPLICATION NUMBER: 60/064,294  
; PRIOR FILING DATE: 1997-11-05

; PRIOR APPLICATION NUMBER: 09/150,786  
; PRIOR FILING DATE: 1998-09-10  
; PRIOR APPLICATION NUMBER: 09/636,399  
; PRIOR FILING DATE: 2000-08-10  
; NUMBER OF SEQ ID NOS: 72  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 2  
; LENGTH: 65  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-409-366-2

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Best Local Similarity 100.0%; Pred. No. 3.2e-35;  
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MRIHYLLFALLFLVLPVPGHGIINTLQKYCRVRGRCAYLSCLPKKEQIGKCTRGR 60

QY 61 KCCRR 65  
Db 61 KCCRR 65

## RESULT 4

US-10-409-532-2  
; Sequence 2, Application US/10409532  
; Publication No. US20030166913A1  
; GENERAL INFORMATION:  
; APPLICANT: Adler, David A.  
; APPLICANT: Holloway, James L.  
; APPLICANT: Baidur, Nand  
; APPLICANT: Beigel-Orme, Stephanie  
; APPLICANT: Sheppard, Paul O.  
; TITLE OF INVENTION: NOVEL BETA-DEFENSINS  
; FILE REFERENCE: 97-44C2  
; CURRENT APPLICATION NUMBER: US/10/409,532  
; CURRENT FILING DATE: 2003-04-07  
; PRIOR APPLICATION NUMBER: US/09/636,399A  
; PRIOR FILING DATE: 2000-08-10  
; PRIOR APPLICATION NUMBER: 60/058,335  
; PRIOR FILING DATE: 1997-10-09  
; PRIOR APPLICATION NUMBER: 60/064,294  
; PRIOR FILING DATE: 1997-11-05  
; PRIOR APPLICATION NUMBER: 09/150,786  
; PRIOR FILING DATE: 1998-09-10  
; PRIOR APPLICATION NUMBER: 09/636,399  
; PRIOR FILING DATE: 2000-08-10  
; NUMBER OF SEQ ID NOS: 72  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 2  
; LENGTH: 65  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-409-532-2

Query Match 100.0%; Score 357; DB 14; Length 65;  
Best Local Similarity 100.0%; Pred. No. 3.2e-35;  
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MRIHYLLFALLFLVLPVPGHGIINTLQKYCRVRGRCAYLSCLPKKEQIGKCTRGR 60

QY 61 KCCRR 65  
Db 61 KCCRR 65

RESULT 5  
US-09-917-340-52  
; Sequence 52, Application US/09917340

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; Patent No. US20020090369A1
; GENERAL INFORMATION:
; APPLICANT: Murphy, Christopher J.
; APPLICANT: McAnulty, Jonathan F.
; APPLICANT: Reid, Ted W.
; TITLE OF INVENTION: Transplant Media
; FILE REFERENCE: TPLANT-06468
; CURRENT APPLICATION NUMBER: US/09/917,340
; CURRENT FILING DATE: 2001-07-29
; PRIOR APPLICATION NUMBER: 60/221,632
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 60/249,602
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/290,932
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 52
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-917-340-52
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Best Local Similarity 100.0%; Pred. No. 3.3e-35;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 MRIHYLLFALLFLFVLPVPGHGGIINTLQKYCRVRGRCAYLSCLPKKEQIGKSTRGR 60
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QY 61 KCCRR 65
Db 61 KCCRR 65
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RESULT 6

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US-09-917-340-72
; Sequence 72, Application US/09917340
; Patent No. US20020090369A1
; GENERAL INFORMATION:
; APPLICANT: Murphy, Christopher J.
; APPLICANT: McAnulty, Jonathan F.
; APPLICANT: Reid, Ted W.
; TITLE OF INVENTION: Transplant Media
; FILE REFERENCE: TPLANT-06468
; CURRENT APPLICATION NUMBER: US/09/917,340
; CURRENT FILING DATE: 2001-07-29
; PRIOR APPLICATION NUMBER: 60/221,632
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 60/249,602
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/290,932
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 72
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-917-340-72
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Query Match 100.0%; Score 357; DB 9; Length 67;
Best Local Similarity 100.0%; Pred. No. 3.3e-35;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 MRIHYLLFALLFLFVLPVPGHGGIINTLQKYCRVRGRCAYLSCLPKKEQIGKSTRGR 60
Db 1 MRIHYLLFALLFLFVLPVPGHGGIINTLQKYCRVRGRCAYLSCLPKKEQIGKSTRGR 60
QY 61 KCCRR 65
Db 61 KCCRR 65
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RESULT 7
US-09-872-852-2
; Sequence 2, Application US/09872852
; Patent No. US20020115602A1
; GENERAL INFORMATION:
; APPLICANT: MCCRAY JR, PAUL B.
; APPLICANT: TACK, BRIAN
; APPLICANT: JIA, HONG PENG
; APPLICANT: SCHUTTE, BRIAN C.
; TITLE OF INVENTION: HUMAN BETA-DEFENSIN-3 (HBD-3), A HIGHLY CATIONIC
; FILE REFERENCE: IOWA:031US
; CURRENT APPLICATION NUMBER: US/09/872,852
; CURRENT FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: 60/208,792
; PRIOR FILING DATE: 2000-06-01
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 2
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-872-852-2
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Query Match 100.0%; Score 357; DB 9; Length 67;
Best Local Similarity 100.0%; Pred. No. 3.3e-35;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 MRIHYLLFALLFLFVLPVPGHGGIINTLQKYCRVRGRCAYLSCLPKKEQIGKSTRGR 60
Db 1 MRIHYLLFALLFLFVLPVPGHGGIINTLQKYCRVRGRCAYLSCLPKKEQIGKSTRGR 60
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QY 61 KCCRR 65
Db 61 KCCRR 65
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RESULT 8

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US-10-091-166B-10
; Sequence 10, Application US/10091166B
; Publication No. US20030143671A1
; GENERAL INFORMATION:
; APPLICANT: Adler, David A.
; APPLICANT: Holloway, James L.
; APPLICANT: Baidur, Nand
; APPLICANT: Beigel-Orme, Stephanie
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: NOVEL BETA-DEFENSINS
; FILE REFERENCE: 97-44D1
; CURRENT APPLICATION NUMBER: US/10/091,166B
; CURRENT FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 09/636,399
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: US 09/344,097
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 09/150,786
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: US 60/064,294
; PRIOR FILING DATE: 1997-11-05
; PRIOR APPLICATION NUMBER: US 60/058,335
; PRIOR FILING DATE: 1997-09-10
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-091-166B-10
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Query Match          100.0%; Score 357; DB 14; Length 67;
Best Local Similarity 100.0%; Pred. No. 3.3e-35;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MRIHYLLFALLFLFLVPGHGGIINTLQKYYCVRVGRGCAVLSCLPKEEQIGKCGSTRGR 60

QY 61 KCCRR 65
   |||||
Db 61 KCCRR 65

RESULT 9
US-10-272-121-10
; Sequence 10, Application US/10272121
; Publication No. US20030157638A1
; GENERAL INFORMATION:
; APPLICANT: Adler, David A.
; APPLICANT: Holloway, James L.
; APPLICANT: Baidur, Nand
; APPLICANT: Beigel-Orme, Stephanie
; APPLICANT: Shepard, Paul O.
; TITLE OF INVENTION: NOVEL BETA-DEFENSINS
; FILE REFERENCE: 97-44D2
; CURRENT APPLICATION NUMBER: US/10/272,121
; PRIOR FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US 09/636,399
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: US 09/344,097
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 09/150,786
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: US 60/064,294
; PRIOR FILING DATE: 1997-11-05
; PRIOR APPLICATION NUMBER: US 60/058,335
; PRIOR FILING DATE: 1997-09-10
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-272-121-10

Query Match          100.0%; Score 357; DB 14; Length 67;
Best Local Similarity 100.0%; Pred. No. 3.3e-35;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRIHYLLFALLFLFLVPGHGGIINTLQKYYCVRVGRGCAVLSCLPKEEQIGKCGSTRGR 60
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Db 1 MRIHYLLFALLFLFLVPGHGGIINTLQKYYCVRVGRGCAVLSCLPKEEQIGKCGSTRGR 60

QY 61 KCCRR 65
   |||||
Db 61 KCCRR 65

RESULT 10
US-10-409-366-10
; Sequence 10, Application US/10409366
; Publication No. US20030166912A1
; GENERAL INFORMATION:
; APPLICANT: Adler, David A.
; APPLICANT: Holloway, James L.
; APPLICANT: Baidur, Nand
; APPLICANT: Beigel-Orme, Stephanie
; APPLICANT: Shepard, Paul O.
; TITLE OF INVENTION: NOVEL BETA-DEFENSINS
; FILE REFERENCE: 97-44C2
; CURRENT APPLICATION NUMBER: US/10/409,366
; CURRENT FILING DATE: 2003-04-07
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; PRIOR APPLICATION NUMBER: US/09/636,399A
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 60/058,335
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/064,294
; PRIOR FILING DATE: 1997-11-05
; PRIOR APPLICATION NUMBER: 09/150,786
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 09/636,399
; PRIOR FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-409-366-10

Query Match          100.0%; Score 357; DB 14; Length 67;
Best Local Similarity 100.0%; Pred. No. 3.3e-35;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRIHYLLFALLFLFLVPGHGGIINTLQKYYCVRVGRGCAVLSCLPKEEQIGKCGSTRGR 60
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Db 1 MRIHYLLFALLFLFLVPGHGGIINTLQKYYCVRVGRGCAVLSCLPKEEQIGKCGSTRGR 60

QY 61 KCCRR 65
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Db 61 KCCRR 65

RESULT 11
US-10-409-532-10
; Sequence 10, Application US/10409532
; Publication No. US20030166913A1
; GENERAL INFORMATION:
; APPLICANT: Adler, David A.
; APPLICANT: Holloway, James L.
; APPLICANT: Baidur, Nand
; APPLICANT: Beigel-Orme, Stephanie
; APPLICANT: Shepard, Paul O.
; TITLE OF INVENTION: NOVEL BETA-DEFENSINS
; FILE REFERENCE: 97-44C2
; CURRENT APPLICATION NUMBER: US/10/409,532
; PRIOR FILING DATE: 2003-04-07
; PRIOR APPLICATION NUMBER: US/09/636,399A
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 60/058,335
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/064,294
; PRIOR FILING DATE: 1997-11-05
; PRIOR APPLICATION NUMBER: 09/150,786
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 09/636,399
; PRIOR FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-409-532-10

Query Match          100.0%; Score 357; DB 14; Length 67;
Best Local Similarity 100.0%; Pred. No. 3.3e-35;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRIHYLLFALLFLFLVPGHGGIINTLQKYYCVRVGRGCAVLSCLPKEEQIGKCGSTRGR 60
   |||||
Db 1 MRIHYLLFALLFLFLVPGHGGIINTLQKYYCVRVGRGCAVLSCLPKEEQIGKCGSTRGR 60

QY 61 KCCRR 65
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Db 61 KCCRR 65
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Db 61 KCCR 65

## RESULT 12

US-09-872-852-4  
; Sequence 4, Application US/09872852  
; Patent No. US20020115602A1  
; GENERAL INFORMATION:  
; APPLICANT: MCCRAY JR, PAUL B.  
; APPLICANT: TACK, BRIAN  
; APPLICANT: JIA, HONG PENG  
; APPLICANT: SCHUTTE, BRIAN C.  
; TITLE OF INVENTION: HUMAN BETA-DEFENSIN-3 (HBD-3), A HIGHLY CATIONIC  
; TITLE OF INVENTION: BETA-DEFENSIN ANTIMICROBIAL PEPTIDE  
; FILE REFERENCE: IOWA:031US  
; CURRENT APPLICATION NUMBER: US/09/872,852  
; CURRENT FILING DATE: 2001-06-01  
; PRIOR APPLICATION NUMBER: 60/208,792  
; PRIOR FILING DATE: 2000-06-01  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 45  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: Peptide  
US-09-872-852-4

Query Match 67.2%; Score 240; DB 9; Length 45;  
Best Local Similarity 100.0%; Pred. No. 2.3e-21;  
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 GIINTLQKYYCVRVGGRCAYLSCLPKKEQIGKCGSTRGRKCCR 65  
Db 1 GIINTLQKYYCVRVGGRCAYLSCLPKKEQIGKCGSTRGRKCCR 43

## RESULT 13

US-10-332-765-27  
; Sequence 27, Application US/10332765  
; Publication No. US20040116652A1  
; GENERAL INFORMATION:  
; APPLICANT: Forsmann, Wolf-Georg  
; APPLICANT: Conejo-Garcia, Jose-Ramon  
; APPLICANT: Adermann, Knut  
; TITLE OF INVENTION: Method for Producing and Using Novel Human Defensins as Biologics  
; TITLE OF INVENTION: Active Proteins for Treating Infections and other Illnesses  
; FILE REFERENCE: 022584us  
; CURRENT APPLICATION NUMBER: US/10/332,765  
; CURRENT FILING DATE: 2003-01-13  
; PRIOR APPLICATION NUMBER: DE10033505.5  
; PRIOR FILING DATE: 2000-07-11  
; NUMBER OF SEQ ID NOS: 78  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 27  
; LENGTH: 44  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-332-765-27

Query Match 65.5%; Score 234; DB 16; Length 44;  
Best Local Similarity 100.0%; Pred. No. 1.2e-20;  
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 IINTLQKYYCVRVGGRCAYLSCLPKKEQIGKCGSTRGRKCCR 65  
Db 1 IINTLQKYYCVRVGGRCAYLSCLPKKEQIGKCGSTRGRKCCR 42

RESULT 14  
US-10-091-166B-36

; Sequence 36, Application US/10091166B  
; Publication No. US20030143671A1  
; GENERAL INFORMATION:

; APPLICANT: Adler, David A.  
; APPLICANT: Holloway, James L.  
; APPLICANT: Baidur, Nand  
; APPLICANT: Beigel-Orme, Stephanie  
; APPLICANT: Sheppard, Paul O.  
; TITLE OF INVENTION: NOVEL BETA-DEFENSINS  
; FILE REFERENCE: 97-44D1  
; CURRENT APPLICATION NUMBER: US/10/091,166B  
; CURRENT FILING DATE: 2002-03-05  
; PRIOR APPLICATION NUMBER: US 09/636,399  
; PRIOR FILING DATE: 2000-08-10  
; PRIOR APPLICATION NUMBER: US 09/344,097  
; PRIOR FILING DATE: 1999-06-25  
; PRIOR APPLICATION NUMBER: US 09/150,786  
; PRIOR FILING DATE: 1998-09-10  
; PRIOR APPLICATION NUMBER: US 60/064,294  
; PRIOR FILING DATE: 1997-11-05  
; PRIOR APPLICATION NUMBER: US 60/058,335  
; PRIOR FILING DATE: 1997-09-10  
; NUMBER OF SEQ ID NOS: 72  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 36  
; LENGTH: 48  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Defensin polypeptide  
; FEATURE:  
; NAME/KEY: VARIANT  
; LOCATION: (45)...(45)  
; OTHER INFORMATION: leucine, isoleucine, valine, phenylalanine, or  
; OTHER INFORMATION: methionine  
US-10-091-166B-36

Query Match 64.7%; Score 231; DB 14; Length 48;  
Best Local Similarity 91.5%; Pred. No. 3e-20;  
Matches 43; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 19 PGHGIINTLQKYYCVRVGGRCAYLSCLPKKEQIGKCGSTRGRKCCR 65  
Db 1 PGHGIINTLQKYYCVRVGGRCAYLSCLPKKEQIGKCGSTRGRKCCR 47

## RESULT 15

US-10-272-121-36  
; Sequence 36, Application US/10272121  
; Publication No. US20030157638A1  
; GENERAL INFORMATION:  
; APPLICANT: Adler, David A.  
; APPLICANT: Holloway, James L.  
; APPLICANT: Baidur, Nand  
; APPLICANT: Beigel-Orme, Stephanie  
; APPLICANT: Sheppard, Paul O.  
; TITLE OF INVENTION: NOVEL BETA-DEFENSINS  
; FILE REFERENCE: 97-44D2  
; CURRENT APPLICATION NUMBER: US/10/272,121  
; CURRENT FILING DATE: 2002-10-15  
; PRIOR APPLICATION NUMBER: US 09/636,399  
; PRIOR FILING DATE: 2000-08-10  
; PRIOR APPLICATION NUMBER: US 09/344,097  
; PRIOR FILING DATE: 1999-06-25  
; PRIOR APPLICATION NUMBER: US 09/150,786  
; PRIOR FILING DATE: 1998-09-10  
; PRIOR APPLICATION NUMBER: US 60/064,294  
; PRIOR FILING DATE: 1997-11-05  
; PRIOR APPLICATION NUMBER: US 60/058,335  
; PRIOR FILING DATE: 1997-09-10  
; NUMBER OF SEQ ID NOS: 72  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 36

LENGTH: 48  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Defensin polypeptide  
FEATURE:  
NAME/KEY: VARIANT  
LOCATION: (45)...(45)  
OTHER INFORMATION: leucine, isoleucine, valine, phenylalanine, or  
OTHER INFORMATION: methionine  
US-10-272-121-36

Query Match 64.7%; Score 231; DB 14; Length 48;  
Best Local Similarity 91.5%; Pred. No. 3e-20;  
Matches 43; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 19 PGHGIIINTLQKYCRVRGRCAYLSCLPKKEQIGKSTRGKCCRR 65  
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Db 1 PGHGIIINTLQLYCRVRGRCAYLSCLPKKECTGKWSTRGRKCCR 47

Search completed: October 13, 2004, 14:54:18  
Job time : 132 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 13, 2004, 14:42:17 ; Search time 38 Seconds  
(without alignments)  
113.439 Million cell updates/sec

Title: US-10-272-121-2  
Perfect score: 357  
Sequence: 1 MRIHYLLFALLFLVFPVPG.....LPKEQIGKSTRGRKCCR 65

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA.\*  
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2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep:\*  
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*  
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Pred. NO. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	DB ID	Description
1	357	100.0	65	4	US-09-636-399A-2
2	357	100.0	67	4	US-09-636-399A-10
3	357	100.0	67	4	US-09-917-340-52
4	357	100.0	67	4	US-09-917-340-72
5	231	64.7	48	4	US-09-636-399A-36
6	231	64.7	49	4	US-09-636-399A-35
7	224	62.7	47	4	US-09-636-399A-38
8	224	62.7	48	4	US-09-636-399A-37
9	218	61.1	46	4	US-09-636-399A-40
10	218	61.1	47	4	US-09-636-399A-39
11	210	58.8	45	4	US-09-636-399A-42
12	210	58.8	46	4	US-09-636-399A-41
13	204	57.1	44	4	US-09-636-399A-44
14	204	57.1	45	4	US-09-636-399A-43
15	198	55.5	42	4	US-09-636-399A-22
16	198	55.5	43	4	US-09-636-399A-21
17	198	55.5	43	4	US-09-636-399A-46
18	198	55.5	44	4	US-09-636-399A-20
19	198	55.5	44	4	US-09-636-399A-45
20	194	54.3	41	4	US-09-636-399A-25
21	194	54.3	42	4	US-09-636-399A-24
22	194	54.3	42	4	US-09-636-399A-48
23	194	54.3	43	4	US-09-636-399A-23
24	194	54.3	43	4	US-09-636-399A-47
25	190	53.2	40	4	US-09-636-399A-28
26	190	53.2	41	4	US-09-636-399A-27
27	190	53.2	41	4	US-09-636-399A-50

28	190	53.2	42	4	US-09-636-399A-26	Sequence 26, Appl
29	190	53.2	42	4	US-09-636-399A-49	Sequence 49, Appl
30	184	51.5	39	4	US-09-636-399A-31	Sequence 31, Appl
31	184	51.5	40	4	US-09-636-399A-30	Sequence 30, Appl
32	184	51.5	40	4	US-09-636-399A-52	Sequence 52, Appl
33	184	51.5	41	4	US-09-636-399A-29	Sequence 29, Appl
34	184	51.5	41	4	US-09-636-399A-51	Sequence 51, Appl
35	179	50.1	38	4	US-09-636-399A-34	Sequence 34, Appl
36	179	50.1	39	4	US-09-636-399A-33	Sequence 33, Appl
37	179	50.1	39	4	US-09-636-399A-54	Sequence 54, Appl
38	179	50.1	40	4	US-09-636-399A-32	Sequence 32, Appl
39	179	50.1	40	4	US-09-636-399A-53	Sequence 53, Appl
40	175	49.0	37	4	US-09-636-399A-14	Sequence 14, Appl
41	175	49.0	38	4	US-09-636-399A-18	Sequence 18, Appl
42	175	49.0	38	4	US-09-636-399A-56	Sequence 56, Appl
43	175	49.0	39	4	US-09-636-399A-19	Sequence 19, Appl
44	175	49.0	39	4	US-09-636-399A-55	Sequence 55, Appl
45	172	48.2	36	4	US-09-636-399A-60	Sequence 60, Appl

ALIGNMENTS

RESULT 1  
US-09-636-399A-2  
; Sequence 2, Application US/09636399A  
; Patent No. 6576755  
; GENERAL INFORMATION:  
; APPLICANT: Adler, David A.  
; APPLICANT: Holloway, James L.  
; APPLICANT: Baindur, Nand  
; APPLICANT: Beigel-Orme, Stephanie  
; APPLICANT: Sheppard, Paul O.  
; TITLE OF INVENTION: NOVEL BETA-DEFENSINS  
; FILE REFERENCE: 97-44C2  
; CURRENT APPLICATION NUMBER: US/09/636,399A  
; CURRENT FILING DATE: 2000-08-10  
; PRIOR APPLICATION NUMBER: 60/058,335  
; PRIOR FILING DATE: 1997-10-09  
; PRIOR APPLICATION NUMBER: 60/064,294  
; PRIOR FILING DATE: 1997-11-05  
; PRIOR APPLICATION NUMBER: 09/150,786  
; PRIOR FILING DATE: 1998-09-10  
; PRIOR APPLICATION NUMBER: 09/636,399  
; PRIOR FILING DATE: 2000-08-10  
; NUMBER OF SEQ ID NOS: 72  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 2  
; LENGTH: 65  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-636-399A-2  
  
Query Match 100.0%; Score 357; DB 4; Length 65;  
Best Local Similarity 100.0%; Pred. No. 1.9e-37;  
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 MRIHYLLFALLFLVFPVPGHGIIINTLQKYCRVRGRCAYLSCLPKEQIGKSTRGR 60  
DB 1 MRIHYLLFALLFLVFPVPGHGIIINTLQKYCRVRGRCAYLSCLPKEQIGKSTRGR 60  
QY 61 KCCRR 65  
DB 61 KCCRR 65  
  
RESULT 2  
US-09-636-399A-10  
; Sequence 10, Application US/09636399A  
; Patent No. 6576755  
; GENERAL INFORMATION:  
; APPLICANT: Adler, David A.  
; APPLICANT: Holloway, James L.



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; APPLICANT: Baindur, Nand
; APPLICANT: Beigel-Orme, Stephanie
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: NOVEL BETA-DEFENSINS
; FILE REFERENCE: 97-44C2
; CURRENT APPLICATION NUMBER: US/09/636,399A
; CURRENT FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 60/058,335
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/064,294
; PRIOR FILING DATE: 1997-11-05
; PRIOR APPLICATION NUMBER: 09/150,786
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 09/636,399
; PRIOR FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-636-399A-10
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Query Match          100.0%; Score 357; DB 4; Length 67;
Best Local Similarity 100.0%; Pred. No. 2e-37;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1  MRIHYLLFALLFLFLVPGHGGIINTLQKYCRVRGRCAYLSCLPKKEQIGKSTRGR 60
        |||||
Db       1  MRIHYLLFALLFLFLVPGHGGIINTLQKYCRVRGRCAYLSCLPKKEQIGKSTRGR 60
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QY      61  KCCRR 65
        |||||
Db       61  KCCRR 65
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RESULT 3
US-09-917-340-52
; Sequence 52, Application US/09917340
; Patent No. 6696238
; GENERAL INFORMATION:
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; APPLICANT: Murphy, Christopher J.
; APPLICANT: McAnulty, Jonathan F.
; APPLICANT: Reid, Ted W.
; TITLE OF INVENTION: Transplant Media
; FILE REFERENCE: TPLANT-06468
; CURRENT APPLICATION NUMBER: US/09/917,340
; CURRENT FILING DATE: 2001-07-29
; PRIOR APPLICATION NUMBER: 60/221,632
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 60/249,602
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/290,932
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 52
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-917-340-52
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Query Match          100.0%; Score 357; DB 4; Length 67;
Best Local Similarity 100.0%; Pred. No. 2e-37;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1  MRIHYLLFALLFLFLVPGHGGIINTLQKYCRVRGRCAYLSCLPKKEQIGKSTRGR 60
        |||||
Db       1  MRIHYLLFALLFLFLVPGHGGIINTLQKYCRVRGRCAYLSCLPKKEQIGKSTRGR 60
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QY      61  KCCRR 65
        |||||
Db       61  KCCRR 65
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RESULT 4
US-09-917-340-72
; Sequence 72, Application US/09917340
; Patent No. 6696238
; GENERAL INFORMATION:
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; APPLICANT: Murphy, Christopher J.
; APPLICANT: McAnulty, Jonathan F.
; APPLICANT: Reid, Ted W.
; TITLE OF INVENTION: Transplant Media
; FILE REFERENCE: TPLANT-06468
; CURRENT APPLICATION NUMBER: US/09/917,340
; CURRENT FILING DATE: 2001-07-29
; PRIOR APPLICATION NUMBER: 60/221,632
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 60/249,602
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/290,932
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 72
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-917-340-72
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Query Match          100.0%; Score 357; DB 4; Length 67;
Best Local Similarity 100.0%; Pred. No. 2e-37;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1  MRIHYLLFALLFLFLVPGHGGIINTLQKYCRVRGRCAYLSCLPKKEQIGKSTRGR 60
        |||||
Db       1  MRIHYLLFALLFLFLVPGHGGIINTLQKYCRVRGRCAYLSCLPKKEQIGKSTRGR 60
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QY      61  KCCRR 65
        |||||
Db       61  KCCRR 65
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RESULT 5
US-09-636-399A-36
; Sequence 36, Application US/09636399A
; Patent No. 6576755
; GENERAL INFORMATION:
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; APPLICANT: Adler, David A.
; APPLICANT: Holloway, James L.
; APPLICANT: Baindur, Nand
; APPLICANT: Beigel-Orme, Stephanie
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: NOVEL BETA-DEFENSINS
; FILE REFERENCE: 97-44C2
; CURRENT APPLICATION NUMBER: US/09/636,399A
; CURRENT FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 60/058,335
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/064,294
; PRIOR FILING DATE: 1997-11-05
; PRIOR APPLICATION NUMBER: 09/150,786
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 09/636,399
; PRIOR FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 36
; LENGTH: 48
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Defensin polypeptide
; NAME/KEY: VARIANT
; LOCATION: (45)...(45)
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; OTHER INFORMATION: Xaa is Leu, Ile, Val, Phe, or Met
US-09-636-399A-36

Query Match
Best Local Similarity 64.7%; Score 231; DB 4; Length 48;
Matches 43; Conservativity 0; Mismatches 4; Indels 0; Gaps 0;

QY 19 PGHGGIINTLQKYCYCRVGRGRCVAVLSCLPKKEQIGKCGSTRGRKCCR 65
Db 1 PGHGGIINTLQLYYCRVGRGRCVAVLSCLPKKECIGKMGSTRGRKCCR 47

RESULT 6
US-09-636-399A-35
; Sequence 35, Application US/09636399A
; Patent No. 6576755
; GENERAL INFORMATION:
; APPLICANT: Adler, David A.
; APPLICANT: Holloway, James L.
; APPLICANT: Baidur, Nand
; APPLICANT: Beigel-Orme, Stephanie
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: NOVEL BETA-DEFENSINS
; FILE REFERENCE: 97-44C2
; CURRENT APPLICATION NUMBER: US/09/636,399A
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 60/058,335
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/064,294
; PRIOR FILING DATE: 1997-11-05
; PRIOR APPLICATION NUMBER: 09/150,786
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 09/636,399
; PRIOR FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 35
; LENGTH: 49
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Defensin polypeptide
; NAME/KEY: VARIANT
; LOCATION: (45)...(45)
; OTHER INFORMATION: Xaa is Leu, Ile, Val, Phe, or Met
US-09-636-399A-35

Query Match
Best Local Similarity 64.7%; Score 231; DB 4; Length 49;
Matches 43; Conservativity 0; Mismatches 4; Indels 0; Gaps 0;

QY 19 PGHGGIINTLQKYCYCRVGRGRCVAVLSCLPKKEQIGKCGSTRGRKCCR 65
Db 1 PGHGGIINTLQLYYCRVGRGRCVAVLSCLPKKECIGKMGSTRGRKCCR 47

RESULT 7
US-09-636-399A-38
; Sequence 38, Application US/09636399A
; Patent No. 6576755
; GENERAL INFORMATION:
; APPLICANT: Adler, David A.
; APPLICANT: Holloway, James L.
; APPLICANT: Baidur, Nand
; APPLICANT: Beigel-Orme, Stephanie
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: NOVEL BETA-DEFENSINS
; FILE REFERENCE: 97-44C2
; CURRENT APPLICATION NUMBER: US/09/636,399A
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 60/058,335
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/064,294
```

```
; PRIOR FILING DATE: 1997-11-05
; PRIOR APPLICATION NUMBER: 09/150,786
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 09/636,399
; PRIOR FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 38
; LENGTH: 47
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Defensin polypeptide
; NAME/KEY: VARIANT
; LOCATION: (44)...(44)
; OTHER INFORMATION: Xaa is Leu, Ile, Val, Phe, or Met.
US-09-636-399A-38

Query Match
Best Local Similarity 62.7%; Score 224; DB 4; Length 47;
Matches 42; Conservativity 0; Mismatches 4; Indels 0; Gaps 0;

QY 20 GHGGIINTLQKYCYCRVGRGRCVAVLSCLPKKEQIGKCGSTRGRKCCR 65
Db 1 GHGGIINTLQLYYCRVGRGRCVAVLSCLPKKECIGKMGSTRGRKCCR 46

RESULT 8
US-09-636-399A-37
; Sequence 37, Application US/09636399A
; Patent No. 6576755
; GENERAL INFORMATION:
; APPLICANT: Adler, David A.
; APPLICANT: Holloway, James L.
; APPLICANT: Baidur, Nand
; APPLICANT: Beigel-Orme, Stephanie
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: NOVEL BETA-DEFENSINS
; FILE REFERENCE: 97-44C2
; CURRENT APPLICATION NUMBER: US/09/636,399A
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 60/058,335
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/064,294
; PRIOR FILING DATE: 1997-11-05
; PRIOR APPLICATION NUMBER: 09/150,786
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 09/636,399
; PRIOR FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 37
; LENGTH: 48
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Defensin polypeptide
; NAME/KEY: VARIANT
; LOCATION: (44)...(44)
; OTHER INFORMATION: Xaa is Leu, Ile, Val, Phe, or Met
US-09-636-399A-37

Query Match
Best Local Similarity 62.7%; Score 224; DB 4; Length 48;
Matches 42; Conservativity 0; Mismatches 4; Indels 0; Gaps 0;

QY 20 GHGGIINTLQKYCYCRVGRGRCVAVLSCLPKKEQIGKCGSTRGRKCCR 65
Db 1 GHGGIINTLQLYYCRVGRGRCVAVLSCLPKKECIGKMGSTRGRKCCR 46

RESULT 9
US-09-636-399A-40
```

```
; Sequence 40, Application US/09636399A
; Patent No. 6576755
; GENERAL INFORMATION:
; APPLICANT: Adler, David A.
; APPLICANT: Holloway, James L.
; APPLICANT: Baidur, Nand
; APPLICANT: Beigel-Orme, Stephanie
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: NOVEL BETA-DEFENSINS
; FILE REFERENCE: 97-44C2
; CURRENT APPLICATION NUMBER: US/09/636,399A
; CURRENT FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 60/058,335
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/064,294
; PRIOR FILING DATE: 1997-11-05
; PRIOR APPLICATION NUMBER: 09/150,786
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 09/636,399
; PRIOR FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 40
; LENGTH: 46
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Defensin polypeptide
; NAME/KEY: VARIANT
; LOCATION: (43)...(43)
; OTHER INFORMATION: Xaa is Leu, Ile, Phe, Val, or Met
; US-09-636-399A-40

Query Match          61.1%; Score 218; DB 4; Length 46;
Best Local Similarity 91.1%; Pred. No. 3.2e-20;
Matches 41; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      21 HGGIINTLQKYYCRVGRGRCVAVLSCLPKKEQIGKSTRGRKCCR 65
Db      1 HGGIINTLQLYCYRVGRGRCVAVLSCLPKKECIGKMSTRGRKCCR 45

RESULT 10
US-09-636-399A-39
; Sequence 39, Application US/09636399A
; Patent No. 6576755
; GENERAL INFORMATION:
; APPLICANT: Adler, David A.
; APPLICANT: Holloway, James L.
; APPLICANT: Baidur, Nand
; APPLICANT: Beigel-Orme, Stephanie
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: NOVEL BETA-DEFENSINS
; FILE REFERENCE: 97-44C2
; CURRENT APPLICATION NUMBER: US/09/636,399A
; CURRENT FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 60/058,335
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/064,294
; PRIOR FILING DATE: 1997-11-05
; PRIOR APPLICATION NUMBER: 09/150,786
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 09/636,399
; PRIOR FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 39
; LENGTH: 47
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Defensin polypeptide
; NAME/KEY: VARIANT
; LOCATION: (43)...(43)
; OTHER INFORMATION: Xaa is Leu, Ile, Phe, Val, or Met
; US-09-636-399A-39
```

```
; LOCATION: (43)...(43)
; OTHER INFORMATION: Xaa is Leu, Ile, Val, Phe, or Met
; US-09-636-399A-39

Query Match          61.1%; Score 218; DB 4; Length 47;
Best Local Similarity 91.1%; Pred. No. 3.2e-20;
Matches 41; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      21 HGGIINTLQKYYCRVGRGRCVAVLSCLPKKEQIGKSTRGRKCCR 65
Db      1 HGGIINTLQLYCYRVGRGRCVAVLSCLPKKECIGKMSTRGRKCCR 45

RESULT 11
US-09-636-399A-42
; Sequence 42, Application US/09636399A
; Patent No. 6576755
; GENERAL INFORMATION:
; APPLICANT: Adler, David A.
; APPLICANT: Holloway, James L.
; APPLICANT: Baidur, Nand
; APPLICANT: Beigel-Orme, Stephanie
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: NOVEL BETA-DEFENSINS
; FILE REFERENCE: 97-44C2
; CURRENT APPLICATION NUMBER: US/09/636,399A
; CURRENT FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 60/058,335
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/064,294
; PRIOR FILING DATE: 1997-11-05
; PRIOR APPLICATION NUMBER: 09/150,786
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 09/636,399
; PRIOR FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 42
; LENGTH: 45
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Defensin polypeptide
; NAME/KEY: VARIANT
; LOCATION: (42)...(42)
; OTHER INFORMATION: Xaa is Leu, Ile, Phe, Val, or Met
; US-09-636-399A-42

Query Match          58.8%; Score 210; DB 4; Length 45;
Best Local Similarity 90.9%; Pred. No. 3.1e-19;
Matches 40; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      22 GGIINTLQKYYCRVGRGRCVAVLSCLPKKEQIGKSTRGRKCCR 65
Db      1 GGIINTLQLYCYRVGRGRCVAVLSCLPKKECIGKMSTRGRKCCR 44

RESULT 12
US-09-636-399A-41
; Sequence 41, Application US/09636399A
; Patent No. 6576755
; GENERAL INFORMATION:
; APPLICANT: Adler, David A.
; APPLICANT: Holloway, James L.
; APPLICANT: Baidur, Nand
; APPLICANT: Beigel-Orme, Stephanie
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: NOVEL BETA-DEFENSINS
; FILE REFERENCE: 97-44C2
; CURRENT APPLICATION NUMBER: US/09/636,399A
; CURRENT FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 60/058,335
; PRIOR FILING DATE: 1997-10-09
```

```
; PRIOR APPLICATION NUMBER: 60/064,294
; PRIOR FILING DATE: 1997-11-05
; PRIOR APPLICATION NUMBER: 09/150,786
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 09/636,399
; PRIOR FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 41
; LENGTH: 46
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Defensin polypeptide
; NAME/KEY: VARIANT
; LOCATION: (42)...(42)
; OTHER INFORMATION: Xaa is Leu, Ile, Phe, Val, or Met
; US-09-636-399A-41
```

```
Query Match          58.8%; Score 210; DB 4; Length 46;
Best Local Similarity 90.9%; Pred. No. 3.2e-19;
Matches 40; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
OY      22 GGIINTLQKYCYCRVRRGGRCVAVLSCLPKKEQIGKCGSTRGRKCCRR 65
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB       1 GGIINTLQLYCYCRVRRGGRCVAVLSCLPKKECIGKMGSTRGRKCCRR 44
```

## RESULT 13

```
US-09-636-399A-44
; Sequence 44, Application US/09636399A
; Patent No. 6576755
; GENERAL INFORMATION:
; APPLICANT: Adler, David A.
; APPLICANT: Holloway, James L.
; APPLICANT: Baidur, Nand
; APPLICANT: Beigel-Orme, Stephanie
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: NOVEL BETA-DEFENSINS
; FILE REFERENCE: 97-44C2
; CURRENT APPLICATION NUMBER: US/09/636,399A
; CURRENT FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 60/058,335
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/064,294
; PRIOR FILING DATE: 1997-11-05
; PRIOR APPLICATION NUMBER: 09/150,786
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 09/636,399
; PRIOR FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 44
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Defensin polypeptide
; NAME/KEY: VARIANT
; LOCATION: (41)...(41)
; OTHER INFORMATION: Xaa is Leu, Ile, Phe, Val, or Met
; US-09-636-399A-44
```

```
Query Match          57.1%; Score 204; DB 4; Length 44;
Best Local Similarity 90.7%; Pred. No. 1.7e-18;
Matches 39; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
OY      23 GIIINTLQKYCYCRVRRGGRCVAVLSCLPKKEQIGKCGSTRGRKCCRR 65
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB       1 GIIINTLQLYCYCRVRRGGRCVAVLSCLPKKECIGKMGSTRGRKCCRR 43
```

## RESULT 14

```
US-09-636-399A-43
; Sequence 43, Application US/09636399A
; Patent No. 6576755
; GENERAL INFORMATION:
; APPLICANT: Adler, David A.
; APPLICANT: Holloway, James L.
; APPLICANT: Baidur, Nand
; APPLICANT: Beigel-Orme, Stephanie
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: NOVEL BETA-DEFENSINS
; FILE REFERENCE: 97-44C2
; CURRENT APPLICATION NUMBER: US/09/636,399A
; CURRENT FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 60/058,335
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/064,294
; PRIOR FILING DATE: 1997-11-05
; PRIOR APPLICATION NUMBER: 09/150,786
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 09/636,399
; PRIOR FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 43
; LENGTH: 45
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Defensin polypeptide
; NAME/KEY: VARIANT
; LOCATION: (41)...(41)
; OTHER INFORMATION: Xaa is Leu, Ile, Val, Phe, or Met
; US-09-636-399A-43
```

```
Query Match          57.1%; Score 204; DB 4; Length 45;
Best Local Similarity 90.7%; Pred. No. 1.7e-18;
Matches 39; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
OY      23 GIIINTLQKYCYCRVRRGGRCVAVLSCLPKKEQIGKCGSTRGRKCCRR 65
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB       1 GIIINTLQLYCYCRVRRGGRCVAVLSCLPKKECIGKMGSTRGRKCCRR 43
```

## RESULT 15

```
US-09-636-399A-22
; Sequence 22, Application US/09636399A
; Patent No. 6576755
; GENERAL INFORMATION:
; APPLICANT: Adler, David A.
; APPLICANT: Holloway, James L.
; APPLICANT: Baidur, Nand
; APPLICANT: Beigel-Orme, Stephanie
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: NOVEL BETA-DEFENSINS
; FILE REFERENCE: 97-44C2
; CURRENT APPLICATION NUMBER: US/09/636,399A
; CURRENT FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 60/058,335
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/064,294
; PRIOR FILING DATE: 1997-11-05
; PRIOR APPLICATION NUMBER: 09/150,786
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 09/636,399
; PRIOR FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 22
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Defensin polypeptide
```



US-09-636-399A-22

Query Match 55.5%; Score 198; DB 4; Length 42;  
Best Local Similarity 90.5%; Pred. No. 9e-18;  
Matches 38; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 24 IINTLQKYYCRVYRGRCAYLSCLPKKEQIGKSTRGRKCCRR 65  
Db 1 IINTLQKYYCRVYRGRCAYLSCLPKKEQIGKSTRGRKCCRR 42

Search completed: October 13, 2004, 14:52:11  
Job time : 49 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 13, 2004, 14:33:32 ; Search time 161 Seconds  
(without alignments)  
144.829 Million cell updates/sec

Title: US-10-272-121-2

Perfect score: 357  
Sequence: 1 MRIHYLLFALLFLFVFPVPG.....LPKEEQIGKSTGRKCCR 65

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_23Sep04:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	357	100.0	65	2	AAV07243	Aay07243 Beta-defe
2	357	100.0	67	2	AAV07244	Aay07244 Beta-defe
3	357	100.0	67	3	AAI10602	Aab10602 Human SAP
4	357	100.0	67	5	AAU09707	Aau09707 Human bet
5	357	100.0	67	5	AAU91016	Aau91016 Transplan
6	357	100.0	67	5	AAU91036	Aau91036 Transplan
7	357	100.0	67	5	AAO17768	Aao17768 Human bet
8	357	100.0	67	8	ADN05995	Adn05995 Antipsori
9	357	100.0	67	3	ADQ08006	Adq08006 Human bet
10	357	100.0	67	3	AAI10600	Aai10600 Human SAP
11	240	67.2	45	5	AAU09709	Aau09709 Human bet
12	240	67.2	45	5	AAO17767	Aao17767 Human bet
13	220	61.6	41	5	AAU09708	Aau09708 Human bet
14	215	60.2	40	5	AAO17766	Aao17766 Human bet
15	201	56.3	35	6	ABR43502	AbR43502 Human bet
16	201	56.3	37	6	ABR43580	AbR43580 Human bet
17	180	50.4	40	7	ADG25620	Adg25620 Human hBD
18	177	49.6	31	5	AAU49576	Aau49576 Human bet
19	177	49.6	31	5	AAU49572	Aau49572 Human bet
20	177	49.6	31	5	AAO17765	Aao17765 Human bet
21	173	48.5	32	3	AAI10621	Aai10621 Human SAP
22	163	45.7	35	6	ABR43503	AbR43503 Mouse bet
23	163	45.7	51	2	AAI12039	Aai12039 Human S'
24	138	38.7	27	5	AAO17781	Aao17781 Human bet
25	138	38.7	27	5	AAO17773	Aao17773 Human bet

26	135	37.8	64	5	AAU91048	Aau91048 Transplan
27	133	37.3	64	2	AAW81071	Aaw81071 Amino aci
28	133	37.3	64	5	AAU91049	Aau91049 Transplan
29	133	37.3	64	6	ADA83836	Ada83836 Human DEF
30	133	37.3	64	8	ADJ75574	Adj75574 Marker ge
31	133	37.3	64	8	ADN04285	Adn04285 Antipsori
32	133	37.3	64	8	ADQ07993	Adq07993 Human bet
33	126	35.3	24	5	AAO17774	Aao17774 Human bet
34	118	33.1	22	5	AAO17772	Aao17772 Human bet
35	116.5	32.6	63	4	AAE02126	Aae02126 Mouse bet
36	112	31.4	19	5	AAO17770	Aao17770 Human bet
37	108	30.3	64	2	AAI86894	Aai86894 Prepro-LA
38	108	30.3	64	5	AAU90965	Aau90965 Transplan
39	106	29.7	64	2	AAI24332	Aai24332 Tracheal
40	106	29.7	64	2	AAE66205	Aae66205 Bovine tr
41	106	29.7	64	2	AAE66204	Aae66204 Bovine tr
42	106	29.7	64	2	AAW69696	Aaw69696 Human tra
43	102.5	28.7	63	4	AAE02122	Aae02122 Mouse zam
44	100	28.0	64	5	AAU91052	Aau91052 Transplan
45	100	28.0	65	2	AAI86896	Aai86896 Prepro-LA

ALIGNMENTS

RESULT 1  
AAV07243  
ID AAV07243 standard; protein; 65 AA.  
AC AAV07243;  
DT 06-JUL-1999 (first entry)  
DE Beta-defensin family member zamp1.  
KW Human; zamp1; beta-defensin; bacterium; fungus; virus; inflammation;  
KW tissue damage; immune response; AIDS; chemotherapy; melanocortin;  
KW antibody; ion flux; cytotoxic activity; mammalian cell.  
XX  
XX Homo sapiens.  
XX OS  
XX PN WO9913080-A1.  
XX PD 18-MAR-1999.  
XX PF 10-SEP-1998; 98WO-US019222.  
XX PR 10-SEP-1997; 97US-0058335P.  
XX PR 10-SEP-1997; 97US-00926529.  
XX PR 05-NOV-1997; 97US-0064294P.  
XX PR 05-NOV-1997; 97US-00964687.  
XX PA (ZYMO ) ZYMOGENETICS INC.  
XX PI Adler D, Holloway JL, Bairdur N, Beigel S;  
XX WPI; 1999-215064/18.  
XX DR N-PSDB; AAX29985.  
XX PT New zamp1 polypeptide and polynucleotide, human beta-defensins - useful  
XX PT as diagnostic reagents and for treatment of microbial infections, and  
XX PT AIDS.  
XX PS Claim 1; Page 70; 79pp; English.  
XX CC This sequence represents the human zamp1 protein which is a member of the  
XX CC beta-defensin protein family. Zamp1 protein is useful as a pharmaceutical  
XX CC composition, useful for treatment of e.g. bacterial, fungal and viral  
XX CC infections. They are also useful pro-inflammatory, for treating chronic  
XX CC tissue damage, and for stimulating the immune response, for treatment of  
XX CC AIDS or chemotherapy patients. Zamp1 polypeptides and antibodies are  
XX CC useful for studying activity of the melanocortin family, studying ion  
XX CC flux in cell culture, and studying cytotoxic activity against mammalian

CC cells in culture, by incubation with the cells. Zamp1 polypeptides are  
CC especially useful for studying epithelial defensin induction in cell  
CC culture when exposed to pathogenic stimuli

XX Sequence 65 AA;

Query Match  
Best Local Similarity 100.0%; Score 357; DB 2; Length 65;  
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MRHYLLFALLFLFLVPVPGHGIINTLQKYCYCRVGRCAVLSCLPKKEQIGKSTRGR 60  
DB 1 MRHYLLFALLFLFLVPVPGHGIINTLQKYCYCRVGRCAVLSCLPKKEQIGKSTRGR 60

OY 61 KCCRR 65  
DB 61 KCCRR 65

RESULT 2  
AAY07244  
ID AAY07244 standard; protein; 67 AA.

XX AAY07244;

DT 06-JUL-1999 (first entry)

DE Beta-defensin family member zamp1.

KW Human; zamp1; beta-defensin; bacterium; fungus; virus; inflammation;  
KW tissue damage; immune response; AIDS; chemotherapy; melanocortin;  
KW antibody; ion flux; cytotoxic activity; mammalian cell.

OS Homo sapiens.

PN WO9913080-A1.

PD 18-MAR-1999.

PF 10-SEP-1998; 98WO-US019222.

PR 10-SEP-1997; 97US-0058335P.

PR 10-SEP-1997; 97US-00926529.

PR 05-NOV-1997; 97US-0064294P.

PR 05-NOV-1997; 97US-00964687.

PI (ZYMO ) ZYMOGENETICS INC.

PI Adler D, Holloway JL, Baidur N, Beigel S;

DR WPI; 1999-215064/18.

DR N-PSDB; AAX29986.

PT New zamp1 polypeptide and polynucleotide, human beta-defensins - useful  
PT as diagnostic reagents and for treatment of microbial infections, and  
PT AIDS.

PS Claim 1; Page 73; 79pp; English.

XX This sequence represents the human zamp1 protein which is a member of the  
CC beta-defensin protein family. Zamp1 protein is useful as a pharmaceutical  
CC composition, useful for treatment of e.g. bacterial, fungal and viral  
CC infections. They are also useful pro-inflammatory, for treating chronic  
CC tissue damage, and for stimulating the immune response, for treatment of  
CC AIDS or chemotherapy patients. Zamp1 polypeptides and antibodies are  
CC useful for studying activity of the melanocortin family, studying ion  
CC flux in cell culture, and studying cytotoxic activity against mammalian  
CC cells in culture, by incubation with the cells. Zamp1 polypeptides are  
CC especially useful for studying epithelial defensin induction in cell  
CC culture when exposed to pathogenic stimuli

XX Sequence 67 AA;

Query Match  
Best Local Similarity 100.0%; Score 357; DB 2; Length 67;  
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MRHYLLFALLFLFLVPVPGHGIINTLQKYCYCRVGRCAVLSCLPKKEQIGKSTRGR 60  
DB 1 MRHYLLFALLFLFLVPVPGHGIINTLQKYCYCRVGRCAVLSCLPKKEQIGKSTRGR 60

OY 61 KCCRR 65  
DB 61 KCCRR 65

RESULT 3  
AAB10602  
ID AAB10602 standard; protein; 67 AA.

XX AAB10602;

DT 08-JAN-2001 (first entry)

DE Human SAP-3 pre-protein.

KW SAP-2; SAP-3; human; antibiotic; antibacterial; antifungal; antiviral;  
KW treatment; microbial infection; wound dressing; diagnostic reagent.

OS Homo sapiens.

PN WO200046245-A2.

PD 10-AUG-2000.

PF 01-FEB-2000; 2000WO-EP000776.

PR 01-FEB-1999; 99DE-01005128.

PR 08-OCT-1999; 99DE-01049436.

PI (SCHD ) SCHERING AG.

PI Christophers E, Harder J, Schroeder J;

DR WPI; 2000-514948/46.

DR N-PSDB; AAA71755.

PT New human antibiotic peptides, useful for treating microbial infections,  
PT particularly when incorporated in wound dressings, also related nucleic  
PT acid.

PS Claim 4; Page 39; 41pp; German.

XX This invention describes the novel active, mature human proteins (I) SAP-  
CC 2 and SAP-3 which have antibiotic, antibacterial, antifungal and  
CC antiviral activity. (I), and their precursors, are useful for treating or  
CC preventing microbial infections (caused by bacteria, fungi or viruses),  
CC particularly where they (or human cells expressing them) are included in  
CC wound dressings, and to produce specific antibodies (Ab) or their  
CC fragments. Ab are used as diagnostic reagents, e.g. to detect a  
CC deficiency of (I) or the presence of a (I) variant. This sequence  
CC represents the human SAP-3 protein described in the method of the  
CC invention

XX Sequence 67 AA;

Query Match  
Best Local Similarity 100.0%; Score 357; DB 3; Length 67;  
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MRHYLLFALLFLFLVPVPGHGIINTLQKYCYCRVGRCAVLSCLPKKEQIGKSTRGR 60  
DB 1 MRHYLLFALLFLFLVPVPGHGIINTLQKYCYCRVGRCAVLSCLPKKEQIGKSTRGR 60

OY 61 KCCRR 65  
DB 61 KCCRR 65

Db 61 KCCRR 65

RESULT 4  
AAU09707 standard; protein; 67 AA.

AC AAU09707;

DT 26-MAR-2002 (first entry)

DE Human beta-defensin-3 (HBD-3).

KW Human; antimicrobial peptide; human beta-defensin-3; HBD-3;  
microbial growth; microbial infection; pulmonary infection.

OS Homo sapiens.

PN WO200192309-A2.

PD 06-DEC-2001.

PF 01-JUN-2001; 2001WO-US018057.

PR 01-JUN-2000; 2000US-0208792P.

PA (IOWA ) UNIV IOWA RES FOUND.

PI Mcclray PB, Tack B, Jia HP, Schutte BC;

DR WPI; 2002-106302/14.  
N-PSDB; AAS14407.

PT New human beta-defensin 3 peptides and nucleic acids encoding peptides,  
useful for treating or preventing microbial growth or infection, or in  
gene therapy.

PS Claim 1; Page 96; 110pp; English.

CC The present invention relates to the isolation of a novel antimicrobial  
peptide, human beta-defensin-3 (HBD-3). Also described is a method of  
inhibiting growth of a microbe by introducing into a host or environment  
the antimicrobial peptide of the invention. The peptide is useful for  
treating or preventing microbial growth or infections, e.g. pulmonary  
infections when administered by inhalation. The peptide can be applied on  
a work surface or a surgical instrument for the prevention and/or  
suppression of microbial growth. The present sequence represents HBD-3

SQ Sequence 67 AA;

Query Match 100.0%; Score 357; DB 5; Length 67;  
Best Local Similarity 100.0%; Pred. No. 2.9e-36;  
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRHYLLFALLFLFVPGHGIIINTLOKYYCVRVGRCAVLSCLPKKEQIGKSTRGR 60  
Db 1 MRHYLLFALLFLFVPGHGIIINTLOKYYCVRVGRCAVLSCLPKKEQIGKSTRGR 60

QY 61 KCCRR 65  
Db 61 KCCRR 65

RESULT 5  
AAU91016 standard; peptide; 67 AA.

AC AAU91016;

DT 05-JUN-2002 (first entry)

DE Transplant media associated defensin peptide #17.

KW Transplant; antimicrobial peptide; pore forming agent;  
cell surface receptor binding compound; kidney transplant; cardioplegia;  
organ transplant; transplant rejection; defensin.

OS Homo sapiens.

PN WO200209738-A1.

PD 07-FEB-2002.

PF 27-JUL-2001; 2001WO-US023785.

PR 28-JUL-2000; 2000US-0221632P.

PR 17-NOV-2000; 2000US-0249602P.

PR 15-MAY-2001; 2001US-0290932P.

PA (MURP/) MURPHY C J.

PI Murphy CJ, Reid TW, Meanulty JF;

PT Media comprising antimicrobial polypeptides or pore forming agents and/or  
cell surface receptor binding compounds useful for the storage and  
preservation of organs prior to transplant.

PS Claim 8; Page 28; 78pp; English.

CC The invention describes new transplant compositions comprising  
antimicrobial polypeptides or pore forming agents and/or cell surface  
receptor binding compounds. The media is capable of extending the  
preservation period past 72 hours and can provide organs with increased  
functionality upon transplant. animals receiving kidneys stored in the  
media of the present invention for either three or four days had serum  
creatinine levels of less than half of those observed in control animals  
receiving kidneys stored in UW solution (defined in the specification)  
alone. Lower serum creatinine levels are indicative of healthier kidneys  
and a more preferable prognosis for the transplant patient. The media of  
the invention are useful for decreasing the incidence and/or severity of  
delayed graft function in patients receiving transplanted kidneys stored  
and/or treated in the media. The media may also be used in procedures  
such as cardioplegia. It is contemplated that transplant of healthier  
organs leads to a decrease in chronic rejection. This sequence represents  
an antimicrobial defensin peptide studied in the development of the  
transplant media

SQ Sequence 67 AA;

Query Match 100.0%; Score 357; DB 5; Length 67;  
Best Local Similarity 100.0%; Pred. No. 2.9e-36;  
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRHYLLFALLFLFVPGHGIIINTLOKYYCVRVGRCAVLSCLPKKEQIGKSTRGR 60  
Db 1 MRHYLLFALLFLFVPGHGIIINTLOKYYCVRVGRCAVLSCLPKKEQIGKSTRGR 60

QY 61 KCCRR 65  
Db 61 KCCRR 65

RESULT 6  
AAU91036 standard; peptide; 67 AA.

AC AAU91036;

DT 05-JUN-2002 (first entry)

DE Transplant media associated defensin peptide #37.

KW Transplant; antimicrobial peptide; pore forming agent;  
cell surface receptor binding compound; kidney transplant; cardioplegia;



KM organ transplant; transplant rejection; defensin.  
XX  
XX Homo sapiens.  
OS  
XX WO200209738-A1.  
PN  
XX 07-FEB-2002.  
PD  
XX  
XX 27-JUL-2001; 2001WO-US023785.  
PF  
XX 28-JUL-2000; 2000US-0221632P.  
PR 17-NOV-2000; 2000US-0249602P.  
PR 15-MAY-2001; 2001US-0290932P.  
PR  
XX (MURP/) MURPHY C J.  
PA  
XX  
XX PI Murphy CJ, Reid TW, Meanlty JF;  
PI  
XX WPI; 2002-268995/31.  
DR  
XX Media comprising antimicrobial polypeptides or pore forming agents and/or  
PT cell surface receptor binding compounds useful for the storage and  
PT preservation of organs prior to transplant.  
PT  
XX  
XX Claim 8; Page 30; 78pp; English.  
PS  
XX The invention describes new transplant compositions comprising  
CC antimicrobial polypeptides or pore forming agents and/or cell surface  
CC receptor binding compounds. The media is capable of extending the  
CC preservation period past 72 hours and can provide organs with increased  
CC functionality upon transplant. animals receiving kidneys stored in the  
CC media of the present invention for either three or four days had serum  
CC creatinine levels of less than half of those observed in control animals  
CC receiving kidneys stored in UW solution (defined in the specification)  
CC alone. Lower serum creatinine levels are indicative of healthier kidneys  
CC and a more preferable prognosis for the transplant patient. The media of  
CC the invention are useful for decreasing the incidence and/or severity of  
CC delayed graft function in patients receiving transplanted kidneys stored  
CC and/or treated in the media. The media may also be used in procedures  
CC such as cardioplegia. It is contemplated that transplant of healthier  
CC organs leads to a decrease in chronic rejection. This sequence represents  
CC an antimicrobial defensin peptide studied in the development of the  
CC transplant media  
CC  
XX  
SQ Sequence 67 AA;  
  
Query Match 100.0%; Score 357; DB 5; Length 67;  
Best Local Similarity 100.0%; Pred. No. 2.9e-36;  
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 MRIHYLLFALLFLFLVPVPGHGIINTLQKYCYCRVGRCAVLSCLPKEBQIGKCSSTRGR 60  
DB 1 MRIHYLLFALLFLFLVPVPGHGIINTLQKYCYCRVGRCAVLSCLPKEBQIGKCSSTRGR 60  
  
QY 61 KCCRR 65  
DB 61 KCCRR 65  
  
RESULT 7  
AA017768 standard; protein; 67 AA.  
ID AA017768;  
XX  
AC AA017768;  
XX  
DT 30-AUG-2002 (first entry)  
XX  
XX Human beta-defensin-3 derivative #3.  
DE  
XX Human; beta-defensin-3; hBD-3; bacterial infection; gene therapy;  
KM respiratory system; cystic fibrosis; inflammation; urogenital tract;  
KM antibacterial; fungicidal; cytostatic; antiinflammatory; antilulcer;  
KM gastrointestinal tract; septicemia; apoptosis induction; cancer.

XX Homo sapiens.  
OS  
XX WO200240512-A2.  
PN  
XX 23-MAY-2002.  
PD  
XX  
XX 14-NOV-2001; 2001WO-EP013174.  
PF  
XX 14-NOV-2000; 2000DE-01056365.  
PR 30-MAR-2001; 2001DE-01016220.  
PR  
XX (IPFP-) IPF PHARM GMBH.  
PA  
XX  
XX PI Forssmann W, Kluever E, Conejo-Garcia J, Adermann K, Bals R;  
PI Maegerl H;  
XX  
XX WPI; 2002-435959/46.  
DR  
XX New human beta-defensin 3, useful for treating or preventing microbial  
PT infection and tumors, also related nucleic acid.  
PT  
XX  
XX Claim 2; Page 23; 36pp; German.  
PS  
XX The present invention relates to human beta-defensin-3 (hBD-3) and its  
CC derivatives. The peptide, its coding sequence and vectors containing the  
CC coding sequence are useful in (gene) therapy and diagnosis, especially  
CC for preventing or treating a wide range of microbial infections  
CC (particularly Burkholderia cepacia and Pseudomonas aeruginosa in the  
CC respiratory tract, especially in cases of cystic fibrosis, and  
CC Helicobacter pylori, also inflammatory diseases of the gastrointestinal  
CC and urogenital tracts, sepsis and yeast infections), and for inducing  
CC apoptosis for treating malignant melanoma and tumours. The present  
CC sequence is a derivative of human BD-3  
CC  
XX  
SQ Sequence 67 AA;  
  
Query Match 100.0%; Score 357; DB 5; Length 67;  
Best Local Similarity 100.0%; Pred. No. 2.9e-36;  
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 MRIHYLLFALLFLFLVPVPGHGIINTLQKYCYCRVGRCAVLSCLPKEBQIGKCSSTRGR 60  
DB 1 MRIHYLLFALLFLFLVPVPGHGIINTLQKYCYCRVGRCAVLSCLPKEBQIGKCSSTRGR 60  
  
QY 61 KCCRR 65  
DB 61 KCCRR 65  
  
RESULT 8  
ADN05995 standard; protein; 67 AA.  
ID ADN05995  
XX  
AC ADN05995;  
XX  
DT 01-JUL-2004 (first entry)  
XX  
XX Antipsoriatic protein sequence #1157.  
DE  
XX antipsoriatic; gene therapy; psoriasis; diagnosis.  
KM  
XX Homo sapiens.  
OS  
XX WO2004028479-A2.  
PN  
XX 08-APR-2004.  
PD  
XX  
XX 25-SEP-2003; 2003WO-US030907.  
PF  
XX 25-SEP-2002; 2002US-0414006P.  
PR  
XX (GETH ) GENENTECH INC.  
PA

XX Bodary S, Clark H, Jackman J, Schoenfeld J, Williams PM, Wood WI;  
PI Wu TD;  
PI XX  
DR WPI; 2004-305105/28.  
DR N-PSDB; ADN05994.  
XX  
PT New PRO nucleic acid or polypeptide, useful for preparing a  
PT pharmaceutical composition for diagnosing or treating psoriasis in a  
PT mammal.  
XX  
PS Claim 9; SEQ ID NO 2390; 3069pp; English.  
XX  
CC The invention relates to novel polynucleotide and polypeptides for  
CC treating psoriasis or a sequence having at least 80% identity to the  
CC above sequences. The nucleic acid is useful for preparing a composition  
CC for diagnosing or treating psoriasis in a mammal. This sequence  
CC corresponds to one of the polypeptides of the invention.  
XX  
SQ Sequence 67 AA;  
Query Match 100.0%; Score 357; DB 8; Length 67;  
Best Local Similarity 100.0%; Pred. No. 2.9e-36;  
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MRTHYLLFALLFLFLVPVPGHGGIINTLQKYCYCRVGRCAVLSCLPKEEQIGKSTRGR 60  
DB 1 MRTHYLLFALLFLFLVPVPGHGGIINTLQKYCYCRVGRCAVLSCLPKEEQIGKSTRGR 60  
QY 61 KCCRR 65  
DB 61 KCCRR 65  
RESULT 9  
ADQ08006  
ID ADQ08006; standard; protein; 67 AA.  
XX  
AC ADQ08006;  
XX  
DT 23-SEP-2004 (first entry)  
XX  
DE Human beta-defensin-3, HBD-3, SEQ ID 15.  
XX  
KW Anti-HIV; Vaccine; HIV infection; Beta Defensin; BD; human; HBD; HBD-2;  
KW HBD-3; antiviral.  
XX  
OS Homo sapiens.  
XX  
PN WO2004054603-A2.  
XX  
PD 01-JUL-2004.  
XX  
PF 15-DEC-2003; 2003WO-US040233.  
XX  
PR 13-DEC-2002; 2002US-0433099P.  
XX  
PA (UYCA-) UNIV CASE WESTERN RESERVE.  
XX  
PI Weinberg A;  
XX  
DR WPI; 2004-488004/46.  
DR N-PSDB; ADQ08007, ADQ08008, ADQ08009.  
XX  
PT Inhibiting HIV infection in a subject comprises administering human Beta  
PT defensin-2 or human Beta defensin-3 agent or Beta Defensin-inducing  
PT agent.  
XX  
PS Claim 9; Page 10; 63pp; English.  
XX  
CC The present invention relates to a method for inhibiting HIV infection in  
CC a subject. The method comprises administering Beta Defensin (BD) agent or  
CC Beta Defensin-inducing agent e.g. a human BD (HBD) agent such as HBD-2 or

CC HBD-3. The agent is administered in combination with an additional  
CC antiviral agent which targets a portion of the HIV virus consisting of an  
CC HIV protease or an HIV reverse transcriptase. BD are a superfamily of  
CC peptide antibiotics with a characteristic beta-sheet structure stabilised  
CC by two to three intramolecular disulfide bonds. The present sequence is  
CC HBD-3.  
XX  
SQ Sequence 67 AA;  
Query Match 100.0%; Score 357; DB 8; Length 67;  
Best Local Similarity 100.0%; Pred. No. 2.9e-36;  
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MRTHYLLFALLFLFLVPVPGHGGIINTLQKYCYCRVGRCAVLSCLPKEEQIGKSTRGR 60  
DB 1 MRTHYLLFALLFLFLVPVPGHGGIINTLQKYCYCRVGRCAVLSCLPKEEQIGKSTRGR 60  
QY 61 KCCRR 65  
DB 61 KCCRR 65  
RESULT 10  
AAB10600  
ID AAB10600; standard; protein; 45 AA.  
XX  
AC AAB10600;  
XX  
DT 08-JAN-2001 (first entry)  
XX  
DE Human SAP-3 mature protein.  
XX  
KW SAP-2; SAP-3; human; antibiotic; antibacterial; antifungal; antiviral;  
KW treatment; microbial infection; wound dressing; diagnostic reagent.  
XX  
OS Homo sapiens.  
XX  
PN WO200046245-A2.  
XX  
PD 10-AUG-2000.  
XX  
PF 01-FEB-2000; 2000WO-EP000776.  
XX  
PR 01-FEB-1999; 99DE-01005128.  
PR 08-OCT-1999; 99DE-01049436.  
XX  
PA (SCHD ) SCHERING AG.  
XX  
PI Christophers E, Harder J, Schroeder J;  
XX  
DR WPI; 2000-514948/46.  
DR N-PSDB; AAA71753.  
XX  
PT New human antibiotic peptides, useful for treating microbial infections,  
PT particularly when incorporated in wound dressings, also related nucleic  
PT acid.  
XX  
PS Claim 1; Page 37; 41pp; German.  
XX  
CC This invention describes the novel active, mature human proteins (I) SAP-  
CC 2 and SAP-3 which have antibiotic, antibacterial, antifungal and  
CC antiviral activity. (I), and their precursors, are useful for treating or  
CC preventing microbial infections (caused by bacteria, fungi or viruses),  
CC particularly where they (or human cells expressing them) are included in  
CC wound dressings, and to produce specific antibodies (Ab) or their  
CC fragments. Ab are used as diagnostic reagents, e.g. to detect a  
CC deficiency of (I) or the presence of a (I) variant. This sequence  
CC represents the mature human SAP-3 protein described in the method of the  
CC invention  
XX  
SQ Sequence 45 AA;  
Query Match 67.2%; Score 240; DB 3; Length 45;

Best Local Similarity 100.0%; Pred. No. 5.2e-22;  
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 GIINTLQKYCYCRVGRGCAVLSCLPKEEQIGKSTRGRKCCRR 65  
Db 1 GIINTLQKYCYCRVGRGCAVLSCLPKEEQIGKSTRGRKCCRR 43

## RESULT 11

AAU09709  
ID AAU09709 standard; protein; 45 AA.

AC AAU09709;

DT 26-MAR-2002 (first entry)

DE Human beta-defensin-3 (HBD-3) mature protein sequence #2.

KW Human; antimicrobial peptide; human beta-defensin-3; HBD-3;  
KW microbial growth; microbial infection; pulmonary infection.

OS Homo sapiens.

PN WO200192309-A2.

PD 06-DEC-2001.

PF 01-JUN-2001; 2001WO-US018057.

PR 01-JUN-2000; 2000US-0208792P.

PA (IOWA ) UNIV IOWA RES FOUND.

PI McCray PB, Tack B, Jia HP, Schutte BC;

DR WPI; 2002-106302/14.

PT New human beta-defensin 3 peptides and nucleic acids encoding peptides,  
PT useful for treating or preventing microbial growth or infection, or in  
PT gene therapy.

PS Claim 29; Page 98; 110pp; English.

CC The present invention relates to the isolation of a novel antimicrobial  
CC peptide, human beta-defensin-3 (HBD-3). Also described is a method of  
CC inhibiting growth of a microbe by introducing into a host or environment  
CC the antimicrobial peptide of the invention. The peptide is useful for  
CC treating or preventing microbial growth or infections, e.g. pulmonary  
CC infections when administered by inhalation. The peptide can be applied on  
CC a work surface or a surgical instrument for the prevention and/or  
CC suppression of microbial growth. The present sequence represents HBD-3  
CC mature protein sequence #2

XX Sequence 45 AA;

Query Match 67.2%; Score 240; DB 5; Length 45;  
Best Local Similarity 100.0%; Pred. No. 5.2e-22;  
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 GIINTLQKYCYCRVGRGCAVLSCLPKEEQIGKSTRGRKCCRR 65  
Db 1 GIINTLQKYCYCRVGRGCAVLSCLPKEEQIGKSTRGRKCCRR 43

## RESULT 12

AAO17767  
ID AAO17767 standard; peptide; 45 AA.

AC AAO17767;

DT 30-AUG-2002 (first entry)

DE Human beta-defensin-3 derivative #2.

XX Human; beta-defensin-3; hBD-3; bacterial infection; gene therapy;  
KW respiratory system; cystic fibrosis; inflammation; urogenital tract;  
KW antibacterial; fungicide; cytostatic; antiinflammatory; antitumor;  
KW gastrointestinal tract; septicemia; apoptosis induction; cancer.

OS Homo sapiens.

PN WO200240512-A2.

PD 23-MAY-2002.

PF 14-NOV-2001; 2001WO-EP013174.

PR 14-NOV-2000; 2000DE-01056365.

PR 30-MAR-2001; 2001DE-01016220.

PA (IPFP-) IPF PHARM GMBH.

PI Forssmann W, Kluever E, Conejo-Garcia J, Adermann K, Bals R;

PI Maegert H;

DR WPI; 2002-435959/46.

PT New human beta-defensin 3, useful for treating or preventing microbial  
PT infection and tumors, also related nucleic acid.

PS Claim 2; Page 23; 36pp; German.

CC The present invention relates to human beta-defensin-3 (hBD-3) and its  
CC derivatives. The peptide, its coding sequence and vectors containing the  
CC coding sequence are useful in (gene) therapy and diagnosis, especially  
CC for preventing or treating a wide range of microbial infections  
CC (particularly Burkholderia cepacia and Pseudomonas aeruginosa in the  
CC respiratory tract, especially in cases of cystic fibrosis, and  
CC Helicobacter pylori, also inflammatory diseases of the gastrointestinal  
CC and urogenital tracts, sepsis and yeast infections), and for inducing  
CC apoptosis for treating malignant melanoma and tumours. The present  
CC sequence is a derivative of human BD-3

XX Sequence 45 AA;

Query Match 67.2%; Score 240; DB 5; Length 45;  
Best Local Similarity 100.0%; Pred. No. 5.2e-22;  
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 GIINTLQKYCYCRVGRGCAVLSCLPKEEQIGKSTRGRKCCRR 65  
Db 1 GIINTLQKYCYCRVGRGCAVLSCLPKEEQIGKSTRGRKCCRR 43

## RESULT 13

AAU09708  
ID AAU09708 standard; protein; 41 AA.

AC AAU09708;

DT 26-MAR-2002 (first entry)

DE Human beta-defensin-3 (HBD-3) mature protein sequence #1.

KW Human; antimicrobial peptide; human beta-defensin-3; HBD-3;  
KW microbial growth; microbial infection; pulmonary infection.

OS Homo sapiens.

PN WO200192309-A2.

PD 06-DEC-2001.

PF 01-JUN-2001; 2001WO-US018057.

PR 01-JUN-2000; 2000US-0208792P.



XX	(IOWA ) UNIV IOWA RES FOUND.
PA	
XX	
PI	McCraty EB, Tack B, Jia HP, Schutte BC;
XX	
DR	WPI; 2002-106302/14.
XX	
PT	New human beta-defensin 3 peptides and nucleic acids encoding peptides,
PT	useful for treating or preventing microbial growth or infection, or in
PT	gene therapy.
XX	
PS	Claim 28; Page 97; 110pp; English.
XX	
CC	The present invention relates to the isolation of a novel antimicrobial
CC	peptide, human beta-defensin-3 (HBD-3). Also described is a method of
CC	inhibiting growth of a microbe by introducing into a host or environment
CC	the antimicrobial peptide of the invention. The peptide is useful for
CC	treating or preventing microbial growth or infections, e.g. pulmonary
CC	infections when administered by inhalation. The peptide can be applied on
CC	a work surface or a surgical instrument for the prevention and/or
CC	suppression of microbial growth. The present sequence represents HBD-3
CC	mature protein sequence #1
XX	
SQ	Sequence 41 AA;
	Query Match 61.6%; Score 220; DB 5; Length 41;
	Best Local Similarity 100.0%; Pred. No. 1.4e-19; Mismatches 0; Indels 0; Gaps 0;
	Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	27 TLQKYYCRVRGGRCAYLSCLPKKEQIGKCSTRGRKCCR 65
Db	1 TLQKYYCRVRGGRCAYLSCLPKKEQIGKCSTRGRKCCR 39
RESULT 14	
ID	AAO17766 standard; peptide; 40 AA.
AC	AAO17766;
XX	
DT	30-AUG-2002 (first entry)
XX	
DE	Human beta-defensin-3 derivative #1.
XX	
KW	Human; beta-defensin-3; hBD-3; bacterial infection; gene therapy;
KW	respiratory system; cystic fibrosis; inflammation; urogenital tract;
KW	antibacterial; fungicide; cytostatic; antiinflammatory; antidiarr;
KW	gastrointestinal tract; septicemia; apoptosis induction; cancer.
XX	
OS	Homo sapiens.
XX	
PN	WO200240512-A2.
XX	
PD	23-MAY-2002.
XX	
PF	14-NOV-2001; 2001WO-EP013174.
XX	
PR	14-NOV-2000; 2000DE-01056365.
PR	30-MAR-2001; 2001DE-01016220.
XX	
PA	(IPRP-) IPF PHARM GMBH.
XX	
PI	Forsmann W, Kluever E, Conejo-Garcia J, Adermann K, Bals R;
PI	Maegert H;
XX	
DR	WPI; 2002-435959/46.
XX	
XX	New human beta-defensin 3, useful for treating or preventing microbial
PT	infection and tumors, also related nucleic acid.
PT	
PS	Claim 2; Page 23; 36pp; German.
PS	
CC	The present invention relates to human beta-defensin-3 (hBD-3) and its

CC derivatives. The peptide, its coding sequence and vectors containing the  
CC coding sequence are useful in (gene) therapy and diagnosis, especially  
CC for preventing or treating a wide range of microbial infections  
CC (particularly Burkholderia cepacia and Pseudomonas aeruginosa in the  
CC respiratory tract, especially in cases of cystic fibrosis, and  
CC Helicobacter pylori, also inflammatory diseases of the gastrointestinal  
CC and urogenital tracts, sepsis and yeast infections), and for inducing  
CC apoptosis for treating malignant melanoma and tumours. The present  
CC sequence is a derivative of human BD-3

XX  
XX Sequence 40 AA;

Query Match 28 LQKYCVRVGRGRCVLSCLPKKEQIGKCGSTRGRCCOR 65  
Db 1 LQKYCVRVGRGRCVLSCLPKKEQIGKCGSTRGRCCOR 38  
Best Local Similarity 100.0%; Pred. No. 5,6e-19;  
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 15  
ABR43502  
ID ABR43502 standard; peptide; 35 AA.  
XX AC ABR43502;  
XX DT 16-JUL-2003 (first entry)  
XX DE Human beta-defensin peptide DEFB3 SEQ ID NO:7.  
XX KW Beta-defensin; antimicrobial; antibacterial; vaccine; gene therapy;  
XX infection; antibiotic; chromosome 8p23-p22.  
OS Homo sapiens.  
XX WO2003024592-A2.  
XX PD 27-MAR-2003.  
XX PF 23-SEP-2002; 2002WO-US030106.  
XX PR 21-SEP-2001; 2001US-0323991P.  
XX PA (IOWA ) UNIV IOWA RES FOUND.  
XX PI Mccray PB, Schutte BC, Jia HP, Casavant TL, Welch MJ;  
XX WPI; 2003-354585/33.  
XX DR

XX New antimicrobial peptides, beta-defensin, useful for preventing  
PT microbial growth, for treating pulmonary infections, for reducing  
PT resistance to antimicrobials and antibiotics, and for inhibiting  
PT multidrug resistant bacteria.

XX  
XX Claim 1; Page 78; 125pp; English.

XX ABR43496 to ABR43577 represent beta-defensin antimicrobial peptides (I).  
CC (I) have antibacterial activity and can be used in vaccines, and in gene  
CC therapy. (I) can be used for preventing microbial growth, for treating  
CC infections (e.g. pulmonary infections), for reducing resistance to  
CC antimicrobials and antibiotics, and for inhibiting multidrug resistant  
CC bacteria. The antimicrobial peptides may be included in food  
CC preparations, pharmaceutical preparations, medicinal and pharmaceutical  
CC products, cosmetic products, hygienic products, cleaning products and  
CC cleaning agents, as well as to any material to which the peptides could  
CC be sprayed on or adhered to where inhibition of microbial growth on such  
CC material is desired. The antimicrobial peptides and nucleic acids  
CC encoding them may be used in gene therapy. ABR43578 to ABR43610 represent  
CC human beta-defensin peptides given in an example from the present  
XX invention

XX  
XX Sequence 35 AA;



Wed Oct 13 15:08:00 2004

us-10-272-121-2.rag

Page 8

	Query Match	56.3%;	Score 201;	DB 6;	Length 35;	
	Best Local Similarity	100.0%;	Pred. No.	2.6e-17;		
	Matches	35;	Conservative	0;	Mismatches	0; Gaps 0;
Oy	31	YYCVRVGGRCAYLSCLPKKEQIGKCGSTRGRKCRR	65			
Dd	1	YYCVRVGGRCAYLSCLPKKEQIGKCGSTRGRKCRR	35			

Search completed: October 13, 2004, 14:47:11  
Job time : 163 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 13, 2004, 14:50:44 ; Search time 193 Seconds  
(without alignment)  
193.779 Million cell updates/sec

Title: US-10-272-121-2  
Perfect score: 65  
Sequence: 1 MRYHYLFLFLFLVFPVG.....LPKEQIGKCKSTRKRCRR 65

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 1825181 seqs, 575374646 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : UniProt\_02:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	65	100.0	67	1	D103_HUMAN	P81534 homo sapien
2	47	72.3	67	2	Q7PCX4	Q7pcx4 papio anubi
3	43	66.2	64	1	D103_PANTR	Q95j42 pan troglod
4	15	23.1	67	2	Q6SC68	Q6sc68 sus scrofa
5	15	23.1	67	2	AAR88759	Aar88759 sus scrof
6	9	13.8	63	1	BD03_MOUSE	Q9wt10 mus musculu
7	9	13.8	64	2	Q9EPV9	Q9epv9 mus musculu
8	9	13.8	67	1	BD01_CHILA	P83943 chinchilla
9	8	12.3	60	2	Q91V82	Q91v82 mus musculu
10	8	12.3	60	2	Q8R556	Q8r556 mus musculu
11	8	12.3	63	1	BD02_RAT	O88514 rattus norv
12	8	12.3	63	1	BD04_MOUSE	P82019 mus musculu
13	8	12.3	67	2	Q7TNV9	Q7tnv9 mus musculu
14	8	12.3	516	2	Q7P1L5	Q7p1l5 chromobacte
15	7	10.8	51	1	YFMN_BACSU	O06472 bacillus su
16	7	10.8	56	2	Q8R997	Q8r997 thermoanaer
17	7	10.8	63	2	Q91VD6	Q91vd6 mus musculu
18	7	10.8	78	2	Q6XIU6	Q6xlu6 feldmannia
19	7	10.8	78	2	AAR26965	Aar26965 feldmanni
20	7	10.8	87	2	Q75YP3	Q75yp3 nesiohelix
21	7	10.8	87	2	Q75Z16	Q75z16 euhadra lat
22	7	10.8	87	2	Q75Z22	Q75z22 euhadra lat
23	7	10.8	87	2	BAC99163	Bac99163 euhadra 1
24	7	10.8	87	2	BAC99169	Bac99169 euhadra 1
25	7	10.8	87	2	BAC99292	Bac99292 nesioheli
26	7	10.8	91	2	Q76C85	Q76c85 human adeno
27	7	10.8	91	2	Q76EL4	Q76el4 human adeno
28	7	10.8	91	2	Q77V93	Q77v93 human adeno
29	7	10.8	91	2	Q7BG8	Q7bg8 human adeno
30	7	10.8	91	2	Q80IV6	Q80iv6 human adeno
31	7	10.8	91	2	Q9ICD4	Q9icd4 human adeno

32	7	10.8	91	2	Q9JFL9	Q9jfl9 human adeno
33	7	10.8	91	2	Q9JFM2	Q9jfm2 human adeno
34	7	10.8	91	2	Q9JFM5	Q9jfm5 human adeno
35	7	10.8	91	2	BAC82701	Bac82701 human ade
36	7	10.8	91	2	BAC87855	Bac87855 human ade
37	7	10.8	101	1	CY02_CATRO	P25923 catharanthu
38	7	10.8	124	2	Q6MZI1	Q6mzi1 homo sapien
39	7	10.8	124	2	CAB46051	Ca46051 homo sapi
40	7	10.8	125	1	NEU1_HUMAN	P01178 homo sapien
41	7	10.8	125	2	AAH69144	Aah69144 homo sapi
42	7	10.8	173	2	Q12408	Q12408 saccharomyc
43	7	10.8	179	2	Q7GX80	Q7gx80 giardia lam
44	7	10.8	201	2	Q9CDE0	Q9cde0 mycobacteri
45	7	10.8	201	2	Q92RI2	Q92ri2 rhizobium m

ALIGNMENTS

RESULT 1  
D103\_HUMAN STANDARD; PRT; 67 AA.  
ID D103\_HUMAN  
AC P81534; Q8NFG6; Q9NPF6;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 01-OCT-2004 (Rel. 45, Last annotation update)  
DE Beta-defensin 103A precursor (Beta-defensin 3) (DEFB-3) (BD-3) (hBD-3)  
DE (HBD3) (Defensin like protein).  
GN Name=DEFB103A; Synonyms=DEFB103, DEFB3, BD3;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
[1]  
SEQUENCE FROM N.A., SEQUENCE OF 23-67, FUNCTION, TISSUE SPECIFICITY,  
RP INDUCTION, AND MASS SPECTROMETRY.  
RC TISSUE=Keratinocytes, lung epithelial cells, and Tracheal epithelium;  
RX MEDLINE=21101950; PubMed=11085990; DOI=10.1074/jbc.M008557200;  
RA Harder J., Bartels J., Christophers E., Schroeder J.-M.;  
RT "Isolation and characterization of human beta-defensin-3, a novel  
RT human inducible peptide antibiotic."  
RL J. Biol. Chem. 276:5707-5713(2001).  
[2]  
SEQUENCE FROM N.A., AND CHARACTERIZATION.  
RP MEDLINE=21558153; PubMed=11702237; DOI=10.1007/s004410100433;  
RX Conejo-Garcia J.-R., Jaumann F., Schulz S., Krause A.,  
RA Rodriguez-Jimenez J., Forssmann U., Adermann K., Kluever E.,  
RA Voglmeier C., Becker D., Hedrich R., Forssmann W.-G., Bals R.;  
RT "Identification of a novel, multifunctional beta-defensin (human beta-  
RT defensin 3) with specific antimicrobial activity. Its interaction with  
RT plasma membranes of Xenopus oocytes and the induction of macrophage  
RT chemotraction."  
RL Cell Tissue Res. 306:257-264(2001).  
[3]  
SEQUENCE FROM N.A.  
RX MEDLINE=21125233; PubMed=11223260; DOI=10.1016/S0378-1119(00)00569-2;  
RA Jia H.-P., Schutte B.C., Schudy A., Linzmeier R., Guthmiller J.M.,  
RA Johnson G.K., Tack B.F., Miltros J.P., Rosenthal A., Ganz T.,  
RA McCray P.B. Jr.;  
RT "Discovery of new human defensins using a genomics-based approach."  
RL Gene 263:211-218(2001).  
[4]  
SEQUENCE FROM N.A.  
RA Imai Y.;  
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.  
[5]  
SEQUENCE FROM N.A.  
RP Adler D.A., Diamond G., Sheppard P., Holloway J., Presnell S.,  
RA Caspers S., Whitmore T., Fox B., Gosink J., Rixon M., Gao Z.,  
RA Haldeman B., O'Hara P.;  
RT "EST and genomic database mining yield novel human and mouse beta-  
RT defensins."  
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.

RN [6]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Tonsil;  
RA Chen S., He F., Li R.;  
RT "Cloning and expression of Chinese human beta defensin-3";  
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.  
RN [7]  
RP STRUCTURE BY NMR OF 23-67.  
RX MEDLINE=21864161; PubMed=11741980; DOI=10.1074/jbc.M108830200;  
RA Schibli D.J., Hunter H.N., Aseyev V., Starner T.D., Wiencek J.M.,  
McCray P.B. Jr., Tack B.F., Vogel H.J.;  
RT "The solution structures of the human beta-defensins lead to a better  
RT understanding of the potent bactericidal activity of HBD3 against  
RT Staphylococcus aureus";  
RL J. Biol. Chem. 277:8279-8289 (2002).  
CC -1- FUNCTION: Exhibits antimicrobial activity against Gram-positive  
CC bacteria S.aureus and S.pyogenes, Gram-negative bacteria  
CC P.aeruginosa and E.coli and the yeast C.albicans. Kills  
CC multi-resistant S.aureus and vancomycin-resistant E.faecium. No  
CC significant hemolytic activity was observed.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- TISSUE SPECIFICITY: Highly expressed in skin and tonsils, and to a  
CC lesser extent in trachea, uterus, kidney, thymus, adenoid, pharynx  
CC and tongue. Low expression in salivary gland, bone marrow, colon,  
CC stomach, polyp and larynx. No expression in small intestine.  
CC -1- INDUCTION: By infection of bacteria and by interferon gamma.  
CC -1- MASS SPECTROMETRY: MW=5154.59; METHOD=Electrospray; RANGE=23-67;  
CC NOTE=Ref.1.  
CC -1- SIMILARITY: Belongs to the beta-defensin family.  
CC -----  
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CC -----  
DR EMBL; AJ237673; CAC03097.1; -;  
DR EMBL; AF295370; AAG02237.1; -;  
DR EMBL; AF217245; AAF73853.1; -;  
DR EMBL; AB037972; BAB40572.1; -;  
DR EMBL; AF301470; AAG22030.1; -;  
DR EMBL; AF51673; AAM62424.1; -;  
DR PDB; 1KJ6; NMR; A=23-66.  
DR Genew; HGNC:15967; DEFBI03A.  
DR MIM; 606611; -;  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0006965; P:anti-Gram-positive bacterial polypeptide in. . .; TAS.  
DR InterPro; IPR001855; Defensin\_beta.  
DR Pfam; PF00711; Defensin\_beta; 1.  
KW 3D-structure; Antibiotic; Direct protein sequencing; Signal.  
FT SIGNAL 1 22  
FT CHAIN 23 67 Beta-defensin 103A.  
FT DISULFID 33 62  
FT DISULFID 40 55  
FT DISULFID 45 63  
FT CONFLICT 45 45 C -> R (in Ref. 6).  
FT TURN 29 31  
FT TURN 32 36  
FT HELIX 39 41  
FT STRAND 47 48  
FT TURN 49 53  
FT STRAND 61 65  
SQ SEQUENCE 67 AA; 7697 MW; 54266DE1C90D4B65 CRC64;  
Query Match 100.0%; Score 65; DB 1; Length 67;  
Best Local Similarity 100.0%; Pred. No. 2.3e-56;  
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
CY 1 MRIHYLLFALLFLFVVPVPGHGGIINTLQKYYCRVGRGCAVLSCLPKKEQIGKCGSTRGR 60  
Db 1 MRIHYLLFALLFLFVVPVPGHGGIINTLQKYYCRVGRGCAVLSCLPKKEQIGKCGSTRGR 60

QY 61 KCCR 65  
Db 61 KCCR 65  
RESULT 2  
O7PCK4 PRELIMINARY; PRT; 67 AA.  
ID O7PCK4  
AC O7PCK4;  
DT 01-MAR-2004 (TREMBlrel. 26, Created)  
DT 01-MAR-2004 (TREMBlrel. 26, last sequence update)  
DT 01-MAR-2004 (TREMBlrel. 26, last annotation update)  
DE DEFBI03-like protein (Fragment).  
OS Papio anubis (Olive baboon).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
OC Cercopithecinae; Papio.  
OX NCBI\_TaxID=9555;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22619651; PubMed=12734011;  
RA Semple C.A., Rolfe M., Dorin J.R.;  
RT "Duplication and selection in the evolution of primate beta-defensin  
RT genes";  
RL Genome Biol. 4:R31-R31(2003).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Semple C.A.M., Rolfe M., Dorin J.R.;  
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.  
CC -1- MISCELLANEOUS: The sequence shown here is derived from an  
CC EMBL/GenBank/DBJ third party annotation (TPA) entry.  
DR EMBL; BK000557; DAA01350.1; -;  
DR GO; GO:0005576; C:extracellular; IEA.  
DR GO; GO:0006952; P:defense response; IEA.  
DR GO; GO:000613; P:response to pest/pathogen/parasite; IEA.  
DR InterPro; IPR001855; Defensin\_beta.  
DR Pfam; PF00711; Defensin\_beta; 1.  
DR NON TER 67  
SQ SEQUENCE 67 AA; 7669 MW; 543F50570B5D4B65 CRC64;  
Query Match 72.3%; Score 47; DB 2; Length 67;  
Best Local Similarity 100.0%; Pred. No. 1.4e-38;  
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
CY 19 PGHGGIINTLQKYYCRVGRGCAVLSCLPKKEQIGKCGSTRGRKCCR 65  
Db 19 PGHGGIINTLQKYYCRVGRGCAVLSCLPKKEQIGKCGSTRGRKCCR 65  
RESULT 3  
D103\_PANTR STANDARD; PRT; 64 AA.  
ID D103\_PANTR  
AC Q95JD2;  
DT 29-MAR-2004 (Rel. 43, Created)  
DT 29-MAR-2004 (Rel. 43, last sequence update)  
DT 05-JUL-2004 (Rel. 44, last annotation update)  
DE Beta-defensin 103A precursor (Beta-defensin 3) (DEFB-3) (BD-3)  
DE (Fragment).  
GN Name=DEFBI03A; Synonyms=DEFBI03, DEFB3;  
OS Pan troglodytes (Chimpanzee).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.  
OX NCBI\_TaxID=9598;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Skin;  
RA Duits L.A., Langermans J.A.M., Ravensbergen B., Paltansing S.,  
RA Vermeine R.A.W., Hiemstra P.S., Thomas A.W., Nibbering P.H.;  
RT "Expression of chimpanzee (Pan troglodytes) beta-defensin-3";  
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.  
CC -1- FUNCTION: Exhibits antimicrobial activity against Gram-positive  
CC and Gram-negative bacteria (By similarity).

CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- SIMILARITY: Belongs to the beta-defensin family.  
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-----  
DR EMBL; AY033883; AAK61549.1; -  
DR InterPro; IPR001855; Defensin\_beta.  
DR Pfam; PF00711; Defensin\_beta; 1.  
KW Antibiotic; Signal.  
FT SIGNAL 1 22 By similarity.  
FT CHAIN 23 >64 Beta-defensin 103A.  
FT DISULFID 33 62 By similarity.  
FT DISULFID 40 55 By similarity.  
FT DISULFID 45 63 By similarity.  
FT NON\_TER 64 64  
SQ SEQUENCE 64 AA; 7299 MW; 01C90D4B60218DC8 CRC64;  
  
Query Match 66.2%; Score 43; DB 1; Length 64;  
Best Local Similarity 100.0%; Pred. No. 1.3e-34;  
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 MRIHYLLFALLFLVVPVPGHGGINTLQKYCVRVGRCAVL 43  
Db 1 MRIHYLLFALLFLVVPVPGHGGINTLQKYCVRVGRCAVL 43  
  
RESULT 4  
Q6SC68 PRELIMINARY; PRT; 67 AA.  
AC Q6SC68;  
DT 05-JUL-2004 (TReMBLrel. 27, Created)  
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)  
DE Prepro-beta-defensin 3.  
OS Sus scrofa (Pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
OX NCBI\_TaxID=9823;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Sang Y., Zhang G., Ross C.R., Blecha F.;  
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY460575; AAR88759.1; -  
SQ SEQUENCE 67 AA; 7790 MW; 6BC28264846572AC CRC64;  
  
Query Match 23.1%; Score 15; DB 2; Length 67;  
Best Local Similarity 100.0%; Pred. No. 6.3e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 MRIHYLLFALLFLFL 15  
Db 1 MRIHYLLFALLFLFL 15  
  
RESULT 5  
AAR88759 PRELIMINARY; PRT; 67 AA.  
AC AAR88759;  
DT 02-MAR-2004 (TReMBLrel. 27, Created)  
DT 02-MAR-2004 (TReMBLrel. 27, Last sequence update)  
DT 02-MAR-2004 (TReMBLrel. 27, Last annotation update)  
DE Prepro-beta-defensin 3.  
OS Sus scrofa (Pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
OX NCBI\_TaxID=9823;  
RN [1]

RP SEQUENCE FROM N.A.  
RA Sang Y., Zhang G., Ross C.R., Blecha F.;  
RT "Characterization of porcine beta-defensin 3 and synergistic effect of  
RT porcine beta-defensin 1, 2 and 3."  
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY460575; AAR88759.1; -  
SQ SEQUENCE 67 AA; 7790 MW; 6BC28264846572AC CRC64;  
  
Query Match 23.1%; Score 15; DB 2; Length 67;  
Best Local Similarity 100.0%; Pred. No. 6.3e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 MRIHYLLFALLFLFL 15  
Db 1 MRIHYLLFALLFLFL 15  
  
RESULT 6  
BD03\_MOUSE STANDARD; PRT; 63 AA.  
ID BD03\_MOUSE  
AC Q9WTL0;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Beta-defensin 3 precursor (BD-3) (MBD-3).  
GN Name=Defb3; Synonyms=Bd3;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A., FUNCTION, INDUCTION, AND TISSUE SPECIFICITY.  
RC STRAIN=C57BL/6; TISSUE=Lung;  
RX MEDLINE=99307216; PubMed=10377137;  
RA Bales R., Wang X., Meegalla R.L., Wattler S., Weiner D.J., Nehls M.C.,  
RA Wilson J.M.;  
RT "Mouse beta-defensin 3 is an inducible antimicrobial peptide expressed  
RT in the epithelia of multiple organs."  
RL Infect. Immun. 67:3542-3547(1999).  
RN [2]  
RP TISSUE SPECIFICITY.  
RC STRAIN=C57BL/6, 129/SvJ, and FVB; TISSUE=Lung;  
RX MEDLINE=20517883; PubMed=10922379;  
RA Jia H.P., Mowk S.A., Schutte B.C., Lee S.K., Vivado A., Tack B.F.,  
RA Bevins C.L., McCray P.B. Jr.;  
RT "A novel murine beta-defensin expressed in tongue, esophagus, and  
RT trachea."  
RL J. Biol. Chem. 275:33314-33320(2000).  
CC -1- FUNCTION: Antimicrobial activity against Gram-negative bacteria  
CC E. coli and P. aeruginosa.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- TISSUE SPECIFICITY: Highest expression in salivary glands,  
CC epididymis, ovary and pancreas and to a lesser extent in lung,  
CC liver and brain. Low or no expression in skeletal muscle and  
CC tongue.  
CC -1- INDUCTION: By bacterial infection.  
CC -1- SIMILARITY: Belongs to the beta-defensin family. LAP/TAP  
CC subfamily.  
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-----  
DR EMBL; AF093245; AAD29573.1; -  
DR EMBL; AF092929; AAD29572.1; -  
DR HSSP; O15263; 1E4Q.  
DR MGD; MGI:1351612; Defb3.  
DR InterPro; IPR001855; Defensin\_beta.  
DR InterPro; IPR006080; Defensin\_mammal.



```

DR pfam; PF00711; Defensin_beta; 1.
DR SMART; SM00048; DEFSN; 1.
KW Antibiotic; Cleavage on pair of basic residues; Signal.
FT SIGNAL 1 20 Potential.
FT PROPEP 21 22 Potential.
FT CHAIN 23 63 Beta-defensin 3.
FT DISULFID 31 59 By similarity.
FT DISULFID 38 52 By similarity.
FT DISULFID 42 60 By similarity.
SQ SEQUENCE 63 AA; 7126 MW; 9D59BC8AD16EA330 CRC64;

Query Match
Best Local Similarity 13.8%; Score 9; DB 1; Length 63;
Best Local Similarity 100.0%; Pred. No. 0.51;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRIHYLLFA 9
Db 1 MRIHYLLFA 9

RESULT 7
Q9EPV9 PRELIMINARY; PRT; 64 AA.
AC Q9EPV9;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Defensin beta 5.
GN Name=Defb5;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Adler D.A., Hollway J.L., Haldeman B.E., Rixon M., Jaspers S.,
RA Fox B., Gosink J., Sheppard P., Presnell S., Gao Z., Whitmore T.,
RA Stamm M., Laube D., Diamond G.,
RA Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
RL EMBL; AF318068; AAC49340.1; -.
DR MGD; MGI:1933153; Defb5.
SQ SEQUENCE 64 AA; 7087 MW; 6105153157A27B3B CRC64;

Query Match
Best Local Similarity 13.8%; Score 9; DB 2; Length 64;
Best Local Similarity 100.0%; Pred. No. 0.52;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRIHYLLFA 9
Db 1 MRIHYLLFA 9

RESULT 8
BD01_CHILA STANDARD; PRT; 67 AA.
AC P83943;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Beta-defensin 1 precursor (CBD-1).
GN Name=DEFB1; Synonyms=BD1;
OS Chinchilla lanigera (Chinchilla).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriognathi; Chinchillidae;
OC Chinchilla.
OX NCBI_TaxID=34839;
RN [1]
RP SEQUENCE FROM N.A., FUNCTION, TISSUE SPECIFICITY, AND MASS
RP SPECTROMETRY.
RC TISSUE=tongue, and Trachea;
RX PubMed=14936845; DOI=10.1074/jbc.M400499200;
RA Harris R.H., Wilk D., Bevins C.L., Munson R.S. Jr., Bakaletz L.O.;
RT "Identification and characterization of mucosal antimicrobial peptides

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RT expressed by the chinchilla (Chinchilla lanigera) airway.";
RL J. Biol. Chem. 279:20250-20256(2004).
CC -!- FUNCTION: Has antibacterial activity against Gram-positive
CC bacterium S.pneumoniae Serotype 14. Is also active against Gram-
CC negative bacteria M.cattarrhalis 1657, and nontypeable H.influenzae
CC strains 86-028NP and 1128. Has antifungal activity against
CC C.albicans. May have a role in maintaining sterility in the middle
CC ear.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Highly expressed in tongue, nasopharyngeal
CC mucosa and skin, and to a lower extent in the Eustachian tube,
CC lung and trachea.
CC -!- MASS SPECTROMETRY: MW=5123; METHOD=Electrospray; RANGE=23-67;
CC NOTE=Ref.1.
CC -!- SIMILARITY: Belongs to the beta-defensin family.
CC -----
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CC -----
DR EMBL; AY128668; AAM97293.1; -.
DR InterPro; IPR006080; Defensin_mammal.
DR SMART; SM00048; DEFSN; 1.
KW Antibiotic; Fungicide; Signal.
FT SIGNAL 1 22 Potential.
FT CHAIN 23 67 Beta-defensin 1.
FT DISULFID 33 62 By similarity.
FT DISULFID 40 55 By similarity.
FT DISULFID 45 63 By similarity.
SQ SEQUENCE 67 AA; 7676 MW; 30A611CDCCD5BA8D CRC64;

Query Match
Best Local Similarity 13.8%; Score 9; DB 1; Length 67;
Best Local Similarity 100.0%; Pred. No. 0.54;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRIHYLLFA 9
Db 1 MRIHYLLFA 9

RESULT 9
Q91V82 PRELIMINARY; PRT; 60 AA.
ID Q91V82;
AC Q91V82;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Beta-defensin 8 (Beta-defensin 6).
GN Name=Defb8;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Conejo-Garcia J.R., Nehls M.C., Wadtler S., Bals R., Heitland A.,
RA Kluever B., Liepke C., Adermann K., Forssmann W.G.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Krause A.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ300674; CAC44635.1; -.
DR EMBL; AJ300673; CAC44634.1; -.
DR PDB; 1E4R; NMR; A=26-60.
DR MGD; MGI:2654206; Defb8.
DR GO; GO:0042742; P:defense response to bacteria; IDA.

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DR InterPro; IPR001855; Defensin_beta.
DR Pfam; PF00711; Defensin_beta; 1.
SQ SEQUENCE 60 AA; 6760 MW; 7213024CF909A59B CRC64;

Query Match
Best Local Similarity 12.3%; Score 8; DB 2; Length 60;
Matches 8; Conservativity 100.0%; Pred. No. 4.8;
Mismatch 0; Indels 0; Gaps 0;

QY 1 MRLHYLLF 8
DB 1 MRLHYLLF 8

RESULT 10
Q8R556 PRELIMINARY; PRT; 60 AA.
AC Q8R556;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Defensin related peptide.
GN Name=Defb8; Synonyms=Defr1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RX MEDLINE=22213784; PubMed=12226710;
RA Morrison G.M., Rolfe M., Kilanowski F.M., Cross S.H., Dorin J.R.;
RT "Identification and characterisation a novel murine beta defensin
related gene.";
RL Mamm. Genome 13:445-451 (2002).
DR HSSP; O15263; 1FD3.
DR MGD; MGI:2654206; Defb8.
DR GO; GO:0042742; P:defense response to bacteria; IDA.
DR InterPro; IPR001855; Defensin_beta.
DR Pfam; PF00711; Defensin_beta; 1.
SQ SEQUENCE 60 AA; 6820 MW; 3702A95649120351 CRC64;

Query Match
Best Local Similarity 12.3%; Score 8; DB 2; Length 60;
Matches 8; Conservativity 100.0%; Pred. No. 4.8;
Mismatch 0; Indels 0; Gaps 0;

QY 1 MRLHYLLF 8
DB 1 MRLHYLLF 8

RESULT 11
BD02_RAT STANDARD; PRT; 63 AA.
ID BD02_RAT
AC O88514;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Beta-defensin 2 precursor (BD-2) (RBD-2).
GN Name=Defb2;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_Taxid=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar;
RX MEDLINE=99386883; PubMed=10456937;
RA Jia H.P., Willis J.N., Barahmand-Pour F., Nishimura D.,
RA Majlumpali R.K., Wang G., Wiles K., Tack B.F., Bevins C.L.,
RA McCray P.B. Jr.;
RT "Molecular cloning and characterization of rat genes encoding
homologues of human beta-defensins.";
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RL Infect. Immun. 67:4827-4833 (1999).
CC -1- FUNCTION: Has bactericidal activity (By similarity).
CC -1- SUBCELLULAR LOCATION: Secreted (Potential).
CC -1- TISSUE SPECIFICITY: Highly expressed in lung.
CC -1- SIMILARITY: Belongs to the beta-defensin family. LAP/TAP
subfamily.
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DR EMBL; AF068861; AAC28072.1; -.
DR HSSP; O15263; 1E4Q.
DR RGD; 619944; Defb2.
DR InterPro; IPR001855; Defensin_beta.
DR InterPro; IPR006080; Defensin_mammal.
DR Pfam; PF00711; Defensin_beta; 1.
DR SMART; SM00048; DEFSN; I.
KW Antibiotic; Signal.
FT SIGNAL 1 20 Potential.
FT PROPEP 21 ? Potential.
FT CHAIN 22 63 Beta-defensin 2.
FT DISULFID 31 59 By similarity.
FT DISULFID 38 52 By similarity.
FT DISULFID 42 60 By similarity.
SQ SEQUENCE 63 AA; 6946 MW; 826099DE2144ACF4 CRC64;

Query Match
Best Local Similarity 12.3%; Score 8; DB 1; Length 63;
Matches 8; Conservativity 100.0%; Pred. No. 5;
Mismatch 0; Indels 0; Gaps 0;

QY 1 MRLHYLLF 8
DB 1 MRLHYLLF 8

RESULT 12
BD04_MOUSE STANDARD; PRT; 63 AA.
ID BD04_MOUSE
AC P82019;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Beta-defensin 4 precursor (BD-4) (MBD-4).
GN Name=Defb4; Synonyms=Bdef4;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.; TISSUE SPECIFICITY, AND VARIANT PRO-12.
RC STRAIN=C57BL/6; TISSUE=Tongue;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaido I., Oseko N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matcova H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusio V., Chochia C., Corbani L.E., Cousins S.,
RA Dalia E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
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RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawai H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Sempile C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlstedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., W ynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Kono H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.,
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573(2002).
CC -!- FUNCTION: Has bactericidal activity (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).
CC -!- TISSUE SPECIFICITY: Tongue, esophagus and trachea.
CC -!- SIMILARITY: Belongs to the beta-defensin family.
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DR EMBL; AF155882; AAD38852.1; -
DR EMBL; AF287475; AAG02197.1; -
DR EMBL; AF288371; AAG10514.1; -
DR EMBL; AK009306; BAB26207.1; -
DR EMBL; AK009061; BAB26051.1; -
DR HSSP; O15263; 1E4Q.
DR MGD; MGI:1927667; Defb4.
DR InterPro; IPR001855; Defensin_beta.
DR InterPro; IPR006080; Defensin_mammal.
DR Pfam; PF00711; Defensin_beta; 1.
DR SMART; SM00048; DEFSN; 1.
KW Antibiotic; Signal.
FT SIGNAL 1 22 Potential.
FT CHAIN 23 63 Beta-defensin 4.
FT DISULFID 31 59 By similarity.
FT DISULFID 38 52 By similarity.
FT DISULFID 42 60 By similarity.
FT VARIANT 12 12 L->P (in strain FVB).
SQ SEQUENCE 63 AA; 7129 MW; 4C7692ED589EE289 CRC64;

Query Match 12.3%; Score 8; DB 1; Length 63;
Best Local Similarity 100.0%; Pred. No. 5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRIHYLLF 8
DB 1 MRIHYLLF 8

RESULT 13
Q7TNV9 PRELIMINARY; PRT; 67 AA.
AC Q7TNV9;
DT 01-OCT-2003 (Tremblrel. 25, Created)
DT 01-OCT-2003 (Tremblrel. 25, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Beta defensin 14.
GN Name=Defb14;

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OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57Bl/6;
RA Maxwell A.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57Bl/6;
RA Dorin J.R.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ578468; CAEL7665.2; -
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR GO; GO:0009613; P:response to pest/pathogen/parasite; IEA.
DR InterPro; IPR001855; Defensin_beta.
DR Pfam; PF00711; Defensin_beta; 1.
SQ SEQUENCE 67 AA; 7718 MW; EEFF0D93ADF17452 CRC64;

Query Match 12.3%; Score 8; DB 2; Length 67;
Best Local Similarity 100.0%; Pred. No. 5.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 RGRCAVL 43
DB 36 RGRCAVL 43

RESULT 14
Q7PIL5 PRELIMINARY; PRT; 516 AA.
ID Q7PIL5;
AC Q7PIL5;
DT 01-MAR-2004 (Tremblrel. 26, Created)
DT 01-MAR-2004 (Tremblrel. 26, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Hypothetical protein.
GN Ordered locus names=Cv0198;
OS Chromobacterium violaceum.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Chromobacterium.
OX NCBI_TaxId=536;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 12472 / DSM 30191;
RX MEDLINE=22882880; PubMed=14500782;
RA Vasconcelos A.T.R., de Almeida D.F., Hungria M., Guimaraes C.T.,
RA Antonio R.V., Almeida F.C., de Almeida L.G.P., de Almeida R.,
RA Alves-Gomes J.A., Andrade E.M., Araxipe J., de Araujo M.F.F.,
RA Astolfi-Filho S., Azevedo V., Baptista A.U., Bataus L.A.M.,
RA Batista J.S., Belo A., van den Berg C., Bogio M., Bonatto S.,
RA Bordignon J., Brigido M.M., Brito C.A., Brocchi M., Burilly H.A.,
RA Camargo A.A., Cardoso D.D.P., Carneiro N.P., Carraro D.M.,
RA Carvalho C.M.B., Cascardo J.C.M., Cavada B.S., Chueire L.M.O.,
RA Creczynski-Pasa T.B., Cunha-Junior N.C., Fagundes N., Falcão C.L.,
RA Fantinatti F., Farias I.P., Felipe M.S.S., Ferrari L.P., Ferro J.A.,
RA Ferro M.I.T., Franco G.R., Freitas N.S.A., Furlan L.R.,
RA Gazzinelli R.T., Gomes E.A., Goncalves P.R., Grangeiro T.B.,
RA Grattapaglia D., Griesard E.C., Hanna E.S., Jardim S.N., Laurino J.,
RA Leoi L.C.T., Lima L.F.A., Loureiro M.F., Lyra M.C.C.P.,
RA Madeira H.M.F., Manfio G.P., Maranhao A.O., Martins W.S.,
RA di Mauro S.M.Z., de Medeiros S.R.B., Meissner R.V., Moreira M.A.M.,
RA Nascimento F.F., Nicolas M.F., Oliveira J.G., Oliveira S.C.,
RA Paixao R.F.C., Parente J.A., Pedrosa F.O., Pena S.D.J., Pereira J.O.,
RA Pereira M., Pinto L.S.R.C., Pinto L.S., Porto J.I.R., Potrich D.P.,
RA Ramalho-Neto C.E., Reis A.M.M., Rigo L.U., Rondinelli E.,
RA Santos E.B.P., Santos F.R., Schneider M.P.C., Seanez H.N.,
RA Silva A.M.R., da Silva A.L.C., Silva D.W., Silva R., Simoes I.C.,
RA Simon D., Soares C.M.A., Soares R.B.A., Souza E.M., Souza K.R.L.,
RA Souza R.C., Steffens M.B.R., Steindel M., Teixeira S.R., Urmenyi T.,
RA Vettore A., Wasseem R., Zaha A., Simpson A.J.G.;

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"The complete genome sequence of Chromobacterium violaceum reveals  
RT remarkable and exploitable bacterial adaptability.";  
RT Proc. Natl. Acad. Sci. U.S.A. 100:11660-11665(2003).  
DR EMBL; AE016910; AA057877.1; -.  
KW Complete proteome; Hypothetical protein.  
SQ SEQUENCE 516 AA; 54740 MW; EA9B809966AA9ACF CRC64;

Query Match 12.3%; Score 8; DB 2; Length 516;  
Best Local Similarity 100.0%; Pred. No. 24;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 LFFALLFL 13  
Db 410 LFFALLFL 417

RESULT 15  
YFMN\_BACSU STANDARD; PRT; 51 AA.  
AC 006472;  
DT 10-OCT-2003 (Rel. 42, Created)  
DT 10-OCT-2003 (Rel. 42, Last sequence update)  
DT 01-OCT-2004 (Rel. 45, Last annotation update)  
DE Hypothetical protein yfmN.  
GN Name=yfmN; OrderedLocustNames=BSU07410;  
OS Bacillus subtilis.  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
OX NCBI\_TaxID=1423;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=AC327;  
RX MEDLINE=97286547; PubMed=9141694;  
RA Yamamoto H., Uchiyama S., Nugroho F.A., Sekiguchi J.;  
RT "A 23.4 kb segment at the 69 degrees-70 degrees region of the Bacillus  
RL Microbiology 143:1317-1320(1997).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=168;  
RX MEDLINE=98044033; PubMed=9384377; DOI=10.1038/36786;  
RA Kunst F., Ogatawara N., Moszer I., Albertini A.M., Alloni G.,  
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,  
RA Borries R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,  
RA Brouillet S., Brusch C.V., Caldwell B., Capuano V., Carter N.M.,  
RA Choi S.K., Codani J.J., Conneron I.F., Cummings N.J., Daniel R.A.,  
RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,  
RA Entian K.-D., Errington J., Fabret C., Ferrari E., Foulger D.,  
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,  
RA Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,  
RA Hilbert H., Holsappel S., Hosono S., Huilo M.F., Itaya M.,  
RA Jones L.-M., Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M.,  
RA Klein C., Kobayashi Y., Koetter P., Koningsstein G., Krogh S.,  
RA Kumano M., Kurita K., Lapidus A., Lardinois S., Lauber J.,  
RA Lazarevic V., Lee S.M., Levine A., Liu H., Masuda S., Mauel C.,  
RA Medigue C., Medina N., Mellado R.P., Mizuno M., Moesti D., Nakai S.,  
RA Noback M., Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B.,  
RA Park S.H., Parro V., Pohl T.M., Portetelle D., Porwollik S.,  
RA Prescott A.M., Prescan E., Puig P., Purnelle B., Rapoport G.,  
RA Rey M., Reynolds S., Rieger M., Rivolta C., Rocha E., Roche B.,  
RA Rose M., Sadate Y., Sato T., Scallan E., Schleich S., Schroeter R.,  
RA Scoffone F., Sekiguchi J., Sekowska A., Seror S.J., Seror P.,  
RA Shin B.S., Soldo B., Sorokin A., Tacconi E., Takagi T., Takahashi H.,  
RA Takemaru K., Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P.,  
RA Tognoni A., Tosato V., Uchiyama S., Vandenbol M., Vannier F.,  
RA Vassarotti A., Viari A., Wambut R., Wedler E., Wedler H.,  
RA Weitzenegger T., Winters P., Wipat A., Yamamoto H., Yamane K.,  
RA Yasumoto K., Yata K., Yoshida K., Yoshikawa H.F., Zumstein E.,  
RA Yoshikawa H., Danchin A.;  
RT "The complete genome sequence of the Gram-positive bacterium Bacillus  
RL subtilis.";  
CC Nature 390:249-256(1997).

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DR EMBL; D86417; BAA22328.1; -.  
DR EMBL; D86418; BAA20103.1; -.  
DR EMBL; Z99107; CAB12560.1; -.  
DR PIR; E69813; E69813.  
DR Subtilist; BG12965; yfmN.  
KW Complete proteome; Hypothetical protein.  
SQ SEQUENCE 51 AA; 5924 MW; 6DB6A157B1B66030 CRC64;

Query Match 10.8%; Score 7; DB 1; Length 51;  
Best Local Similarity 100.0%; Pred. No. 42;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 43 LSCLPKX 49  
Db 44 LSCLPKX 50

Search completed: October 13, 2004, 15:00:26  
Job time : 195 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 13, 2004, 14:51:25 ; Search time 39 Seconds

(without alignments)  
160.361 Million cell updates/sec

Title: US-10-272-121-2

Perfect score: 65

Sequence: 1 MRIHYLLFALLFLFLVPVG.....LPKEEQIGKCGSTRGRKCCR 65

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : PIR 79:\*\*

1: pirl:\*  
2: pirl2:\*  
3: pirl3:\*  
4: pirl4:\*\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	7	10.8	51	2 E69813	hypothetical prote
2	7	10.8	101	2 JQ0877	cyc02 protein prec
3	7	10.8	125	1 NFMU1	oxytocin / neuroph
4	7	10.8	173	2 S67579	probable membrane
5	7	10.8	201	2 T10017	hypothetical prote
6	7	10.8	258	2 F83207	probable permease
7	7	10.8	302	2 B81696	4-hydroxybenzoate
8	7	10.8	312	2 T08985	hypothetical prote
9	7	10.8	373	2 B90253	high-affinity nick
10	7	10.8	378	2 D70324	hypothetical prote
11	7	10.8	380	2 AG2319	hypothetical prote
12	7	10.8	405	2 F96505	probable nucellin
13	7	10.8	427	2 E83385	hypothetical prote
14	7	10.8	485	2 JQ1957	glucagon receptor
15	7	10.8	512	2 S74561	hypothetical prote
16	7	10.8	602	2 G81654	conserved hypochet
17	7	10.8	602	2 F71496	hypothetical prote
18	7	10.8	683	1 QOBEM8	gene 29 protein -
19	7	10.8	683	2 T42943	hypothetical prote
20	7	10.8	4861	2 S71752	giant protein p619
21	6	9.2	30	2 I58367	gag protein - mous
22	6	9.2	49	2 S02007	protamine I - rabb
23	6	9.2	49	2 T07307	hypothetical prote
24	6	9.2	55	2 A83500	periplasmic nitrat
25	6	9.2	73	2 T03199	hypothetical prote
26	6	9.2	75	2 B81354	probable lipoprote
27	6	9.2	76	2 A28945	neuromedin B precu
28	6	9.2	77	2 A86499	hypothetical prote
29	6	9.2	77	2 A72125	hypothetical prote

30	6	9.2	77	2 AH1279	hypothetical prote
31	6	9.2	77	2 AH1642	hypothetical prote
32	6	9.2	79	2 S42861	hypothetical prote
33	6	9.2	80	2 H75569	hypothetical prote
34	6	9.2	86	2 B37402	neurophysin - babo
35	6	9.2	89	2 I51423	gonadoliberin prec
36	6	9.2	93	2 T44069	hypothetical prote
37	6	9.2	102	2 T10199	hypothetical prote
38	6	9.2	103	2 C75149	hypothetical prote
39	6	9.2	104	2 S53606	NADH2 dehydrogenas
40	6	9.2	105	2 F72614	hypothetical prote
41	6	9.2	113	2 S66967	probable membrane
42	6	9.2	118	2 F90459	hypothetical prote
43	6	9.2	121	2 D97087	hypothetical prote
44	6	9.2	124	2 G75416	hypothetical prote
45	6	9.2	128	2 S26430	hypothetical 14.5k

#### ALIGNMENTS

RESULT 1  
E69813  
hypothetical protein yfmN - Bacillus subtilis  
C/Species: Bacillus subtilis  
C/Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 09-Jul-2004  
C/Accession: E69813  
R/Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berte  
C.; Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch  
A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.  
Nature 390, 249-256, 1997  
A/Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galle  
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F  
Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois  
A/Authors: lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mauee  
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelli  
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon  
A/Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Sero  
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama  
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida,  
A/Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.  
A/Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.  
A/Reference number: A69580; MUID:98044033; PMID:9384377  
A/Accession: E69813  
A/Status: preliminary; nucleic acid sequence not shown; translation not shown  
A/Molecule type: DNA  
A/Residues: 1-51 <KUN>  
A/Cross-references: UNIPROT:O06472; GB:Z99107; GB:Z99108; GB:AL009126; NID:G2633055; PI  
A/Experimental source: strain 168  
C/Genetics:  
A/Gene: yfmN

Query Match 10.8%; Score 7; DB 2; Length 51;  
Best Local Similarity 100.0%; Pred. No. 3.8;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 43 LSCLPKE 49  
Db 44 LSCLPKE 50

RESULT 2  
JQ0877  
cyc02 protein precursor - Madagascar periwinkle  
C/Species: Catharanthus roseus (Madagascar periwinkle)  
C/Date: 12-Feb-1993 #sequence\_revision 12-Feb-1993 #text\_change 09-Jul-2004  
C/Accession: JQ0877  
R/Kodama, H.; Ito, M.; Hattori, T.; Nakamura, K.; Komamine, A.  
Submitted to JIPID, February 1991  
A/Description: Isolation of genes that are preferentially expressed at the G1/S bounda  
A/Reference number: JQ0877  
A/Accession: JQ0877  
A/Molecule type: mRNA

A/Residues: 1-101 <KOD>  
A/Cross-references: UNIPROT:P25923  
A/Experimental source: strain B, cell suspension culture  
C/Genetics:  
A/Gene: cyCO2  
F/1-23/Domain: signal sequence #status predicted <SIG>  
F/24-101/Product: cyCO2 protein #status predicted <MAT>

Query Match 10.8%; Score 7; DB 2; Length 101;  
Best Local Similarity 100.0%; Pred. No. 6.3;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 LFFALLF 12  
Db 9 LFFALLF 15

RESULT 3  
NFHUI  
oxytocin / neurophysin 1 precursor [validated] - human  
N/Alternate names: neurophysin I; prepro-OT-NPI  
N/Contains: neurophysin 1; oxytocin  
C/Species: Homo sapiens (man)  
C/Date: 24-Apr-1984 #sequence\_revision 30-Sep-1987 #text\_change 09-Jul-2004  
C/Accession: A94676; A91352; A94229; A93948; A91292; A37402; I84607; A01440; A01450; B23  
R/Sausville, E.; Carney, D.; Battey, J.  
J. Biol. Chem. 260, 10236-10241, 1985  
A/Title: The human vasopressin gene is linked to the oxytocin gene and is selectively ex  
A/Reference number: A94676; MUID:85261445; PMID:2991279  
A/Accession: A94676  
A/Molecule type: DNA  
A/Residues: 1-99,101-125 <SAN>  
A/Cross-references: UNIPROT:P01178; GB:M1186; NID:g189414; PIDN:AAA98806.1; PID:g386991  
R/Mohr, E.; Hillers, M.; Ivell, R.; Haulica, I.D.; Richter, D.  
FEBS Lett. 193, 12-16, 1985  
A/Title: Expression of the vasopressin and oxytocin genes in human hypothalami.  
A/Reference number: A91352; MUID:86056283; PMID:4065330  
A/Accession: A91352  
A/Molecule type: mRNA  
A/Residues: 80-125 <MOH>  
A/Cross-references: GB:X03173; NID:g35170; PIDN:CAA26936.1; PID:g825699  
R/Light, A.; du Vigneaud, V.  
Proc. Soc. Exp. Biol. Med. 98, 692-696, 1958  
A/Title: On the nature of oxytocin and vasopressin from human pituitary.  
A/Reference number: A94229  
A/Accession: A94229  
A/Molecule type: protein  
A/Residues: 20-28 <LIg>  
R/Chauvet, M.T.; Hurpet, D.; Chauvet, J.; Acher, R.  
Proc. Natl. Acad. Sci. U.S.A. 80, 2839-2843, 1983  
A/Title: Identification of human neurophysins: complete amino acid sequences of MSEL- an  
A/Reference number: A93948; MUID:83221497; PMID:6574452  
A/Accession: A93948  
A/Molecule type: protein  
A/Residues: 32-125 <CHA>  
R/Schlesinger, D.H.; Audhya, T.K.  
FEBS Lett. 128, 325-328, 1981  
A/Title: A comparative study of mammalian neurophysin protein sequences.  
A/Reference number: A91292; MUID:81261248; PMID:7262323  
A/Accession: A91292  
A/Molecule type: protein  
A/Residues: 32-99, 'AA', 102-123, 'L', 125 <SCH>  
R.Ivell, R.; Furuya, K.; Brackmann, B.; Dawood, Y.; Khan-Dawood, F.  
Endocrinology 127, 2990-2996, 1990  
A/Title: Expression of the oxytocin and vasopressin genes in human and baboon gonadal ti  
A/Reference number: A37402; MUID:91065270; PMID:2249637  
A/Accession: A37402  
A/Molecule type: mRNA  
A/Residues: 25-93, 'G', 95-110 <IVE>  
A/Cross-references: GB:M2611; NID:g189416; PIDN:AAA59979.1; PID:g189417  
R/Rebhein, M.; Hillers, M.; Mohr, E.; Ivell, R.; Morley, S.; Schmale, H.; Richter, D.  
Biol. Chem. Hoppe-Seyler 367, 695-704, 1986  
A/Title: The neurohypophyseal hormones vasopressin and oxytocin. Precursor structure, sy

A/Reference number: I45952; MUID:87026235; PMID:3768139  
A/Accession: I84607  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: mRNA  
A/Residues: 1-125 <RES>  
A/Cross-references: GB:M25650; NID:g189410; PIDN:AAA59977.1; PID:g189411  
C/Genetics:  
A/Gene: GDB:OXT; OT  
A/Cross-references: GDB:120253; OMIM:167050  
A/Map position: 20p13-20p13  
A/Introns: 40/3; 108/1  
C/Function:  
A/Description: oxytocin is a posterior pituitary peptide hormone that induces uterine c  
xytocin  
C/Superfamily: oxytocin-neurophysin  
C/Keywords: amidated carboxyl end; hormone; lactation; posterior pituitary  
F/1-19/Domain: signal sequence #status predicted <SIG>  
F/20-28/Product: oxytocin #status experimental <OXN>  
F/32-125/Product: neurophysin 1 #status experimental <NFI>  
F/20-25/Disulfide bonds: #status experimental  
F/28/Modified site: amidated carboxyl end (Gly) (amide in mature form from following gl)  
F/41-85, 44-58, 52-75, 59-65, 92-104, 98-116, 105-110/Disulfide bonds: #status predicted

Query Match 10.8%; Score 7; DB 1; Length 125;  
Best Local Similarity 100.0%; Pred. No. 7.4;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 37 GGRCAVL 43  
Db 95 GGRCAVL 101

RESULT 4  
S67579  
probable membrane protein YDL046w - yeast (Saccharomyces cerevisiae)  
N/Alternate names: hypothetical protein D2699  
C/Species: Saccharomyces cerevisiae  
C/Date: 12-Jul-1996 #sequence\_revision 12-Jul-1996 #text\_change 09-Jul-2004  
C/Accession: S67579  
R/Paulin, L.; Saren, A.M.; Laamanen, P.  
submitted to the Protein Sequence Database, July 1996  
A/Reference number: S67560  
A/Accession: S67579  
A/Molecule type: DNA  
A/Residues: 1-173 <PAU>  
A/Cross-references: UNIPROT:Q12408; EMBL:Z74094; NID:g1431035; PID:e253204; PID:g143103  
A/Experimental source: strain S288C  
C/Genetics:  
A/Gene: MIPS:YDL046w  
A/Cross-references: SGD:S0002204  
A/Map position: 4L  
C/Superfamily: Saccharomyces cerevisiae probable membrane protein YDL046w  
C/Keywords: transmembrane protein  
F/8-24/Domain: transmembrane #status predicted <TM>

Query Match 10.8%; Score 7; DB 2; Length 173;  
Best Local Similarity 100.0%; Pred. No. 9.4;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 LFFALLF 13  
Db 8 LFFALLF 14

RESULT 5  
T10017  
hypothetical protein - Mycobacterium leprae  
C/Species: Mycobacterium leprae  
C/Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 09-Jul-2004  
C/Accession: T10017  
R/Cole, S.T.  
submitted to the EMBL Data Library, August 1997  
A/Reference number: Z16916

A/Accession: T10017  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-201 <COL>  
A/Cross-references: UNIPROT:Q9CDE0; EMBL:Z70722; NID:e1059634; PID:e338507  
C/Genetics:  
A/Note: MBL1770.17c

Query Match 10.8%; Score 7; DB 2; Length 201;  
Best Local Similarity 100.0%; Pred. No. 11;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 LFLFLVP 17  
|||  
Db 75 LFLFLVP 81

## RESULT 6

Probable permease of ABC transporter PA3512 [imported] - Pseudomonas aeruginosa (strain F83207  
C/Species: Pseudomonas aeruginosa  
C/Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 09-Jul-2004  
C/Accession: F83207  
R/Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Bradman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J.; Lory, S.; Olson, M.V.  
Nature 406, 959-964, 2000  
A/Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen  
A/Reference number: A82950; MUID:20437337; PMID:10984043  
A/Accession: F83207  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-258 <STO>  
A/Cross-references: UNIPROT:Q9HY97; GB:AE004771; GB:AE004091; NID:g9949650; PIDN:AA60690  
A/Experimental source: strain PA01  
C/Genetics:  
A/Gene: PA3512  
C/Superfamily: Synecococcus nitrate transport protein nrtB

Query Match 10.8%; Score 7; DB 2; Length 258;  
Best Local Similarity 100.0%; Pred. No. 13;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 ALLFLFL 15  
|||  
Db 13 ALLFLFL 19

## RESULT 7

B81696  
4-hydroxybenzoate octaprenyltransferase TC0492 [imported] - Chlamydia muridarum (strain C/Species: Chlamydia muridarum, Chlamydia trachomatis MoPn  
C/Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 09-Jul-2004  
C/Accession: B81696  
R/Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, C.; Dodson, R.; Gwin, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg, Nucleic Acids Res. 28, 1397-1406, 2000  
A/Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.  
A/Reference number: A81500; MUID:20150255; PMID:10684935  
A/Accession: B81696  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-302 <TET>  
A/Cross-references: UNIPROT:Q9PKH3; GB:AE002318; GB:AE002160; NID:g7190531; PIDN:AAF3933  
A/Experimental source: strain N199 (MoPn)  
C/Genetics:  
A/Gene: TC0492  
C/Superfamily: 4-hydroxybenzoate octaprenyltransferase

Query Match 10.8%; Score 7; DB 2; Length 302;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LFLALLFL 13  
|||  
Db 17 LFLALLFL 23

## RESULT 8

T08985  
hypothetical protein F6G3.120 - Arabidopsis thaliana  
C/Species: Arabidopsis thaliana (mouse-ear cress)  
C/Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 09-Jul-2004  
C/Accession: T08985  
R/Beyan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Mayer, K.F. submitted to the Protein Sequence Database, May 1999  
A/Reference number: Z16520  
A/Accession: T08985  
A/Molecule type: DNA  
A/Residues: 1-312 <BEV>  
A/Cross-references: UNIPROT:Q9SZW2; EMBL:AL078464; GSPDB:GN00062; ATSP:F6G3.120  
A/Experimental source: cultivar Columbia; BAC clone F6G3  
C/Genetics:  
A/Gene: ATSP:F6G3.120  
A/Map position: 4  
A/Introns: 55/1; 94/3; 115/3; 151/3; 168/3; 189/3; 241/3; 264/3; 285/2

Query Match 10.8%; Score 7; DB 2; Length 312;  
Best Local Similarity 100.0%; Pred. No. 15;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 LLFLFLV 16  
|||  
Db 7 LLFLFLV 13

## RESULT 9

B90253  
high-affinity nickel-transport protein (hoxN) hoxN [imported] - Sulfolobus solfataricus  
C/Species: Sulfolobus solfataricus  
C/Date: 24-May-2001 #sequence\_revision 24-May-2001 #text\_change 09-Jul-2004  
C/Accession: B90253  
R/She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Aweyer, M.J.; Chan Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, arett, R.A.; Ragan, M.A.; Sengen, C.W.; Van der Oost, J.  
submitted to GenBank, April 2001  
A/Description: Sulfolobus solfataricus complete genome.  
A/Reference number: A99139  
A/Accession: B90253  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-373 <KUR>  
A/Cross-references: UNIPROT:Q97ZB2; GB:AE006641; NID:g13814199; PIDN:AAK41281.1; GSPDB: A/Genetics:  
A/Gene: hoxN  
C/Superfamily: nickel transport protein YFO2673

Query Match 10.8%; Score 7; DB 2; Length 373;  
Best Local Similarity 100.0%; Pred. No. 17;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 ALLFLFL 15  
|||  
Db 50 ALLFLFL 56

## RESULT 10

D70324  
hypothetical protein aq\_267 - Aquifex aeolicus  
C/Species: Aquifex aeolicus  
C/Date: 08-May-1998 #sequence\_revision 08-May-1998 #text\_change 09-Jul-2004  
C/Accession: D70324  
R/Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; C V.  
Nature 392, 353-358, 1998  
A/Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.



A;Reference number: A70300; MUID:98196666; PMID:9537320  
A;Accession: D70324  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-378 <AQF>  
A;Cross-references: UNIPROT:O66624; GB:AE000681; NID:g2982963; PIDN:AAC06585.1; PID:g298  
A;Experimental source: strain VFS  
C;Genetics:  
A;Gene: aq\_267

Query Match 10.8%; Score 7; DB 2; Length 378;  
Best Local Similarity 100.0%; Pred. No. 17;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LFALEFL 13  
DB 247 LFALEFL 253

RESULT 11  
AG2319  
hypothetical protein all4110 [imported] - Nostoc sp. (strain PCC 7120)  
C;Species: Nostoc sp. PCC 7120  
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120  
C;Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 09-Jul-2004  
C;Accession: AG2319  
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S  
DNA Res. 8, 205-213, 2001  
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana  
A;Reference number: AB1807; MUID:21595285; PMID:11759840  
A;Accession: AG2319  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-380 <KUR>  
A;Cross-references: UNIPROT:Q8YPT1; GB:BA000019; PIDN:BA875809.1; PID:G17133245; GSPDB:G  
A;Experimental source: strain PCC 7120  
C;Genetics:  
A;Gene: all4110  
C;Superfamily: magnesium and cobalt transport protein

Query Match 10.8%; Score 7; DB 2; Length 380;  
Best Local Similarity 100.0%; Pred. No. 17;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 FALLEFL 14  
DB 359 FALLEFL 365

RESULT 12  
P96505  
probable nucleolin [imported] - Arabidopsis thaliana  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004  
C;Accession: P96505  
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, C.  
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;  
ansen, N.F.; Hughes, B.; Huizar, L.  
Nature 408, 816-820, 2000  
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.  
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Malt, R.; Marzalli,  
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,  
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
A;Reference number: A86141; MUID:21016719; PMID:11130712  
A;Accession: P96505  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-405 <STO>  
A;Cross-references: UNIPROT:Q9CGY5; GB:AE005173; NID:G1120822; PIDN:AG31001.1; GSPDB:G  
C;Genetics:

A;Gene: T7023.17  
A;Map position: 1

Query Match 10.8%; Score 7; DB 2; Length 405;  
Best Local Similarity 100.0%; Pred. No. 18;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 LLEFLV 16  
DB 8 LLEFLV 14

RESULT 13  
E83385  
hypothetical protein PA2091 [imported] - Pseudomonas aeruginosa (strain PA01)  
C;Species: Pseudomonas aeruginosa  
C;Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 09-Jul-2004  
C;Accession: E83385  
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; B  
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim  
; Lory, S.; Olson, M.V.  
Nature 406, 959-964, 2000  
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic path  
A;Reference number: A82950; MUID:20437337; PMID:10984043  
A;Accession: E83385  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-427 <STO>  
A;Cross-references: UNIPROT:Q91224; GB:AE004636; GB:AE004091; NID:G9948093; PIDN:AG054  
A;Experimental source: strain PA01  
C;Genetics:  
A;Gene: PA2091  
C;Superfamily: hypothetical protein c0103

Query Match 10.8%; Score 7; DB 2; Length 427;  
Best Local Similarity 100.0%; Pred. No. 19;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 YLFLAL 11  
DB 122 YLFLAL 128

RESULT 14  
JQ1957  
glucagon receptor - rat  
N;Alternate names: GUP-1 receptor homolog, hepatic  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 09-Jul-2004  
C;Accession: JQ1957; A46211; S29689  
R;Svoboda, M.; Ciccarelli, E.; Tasty, M.; Cauvin, A.; Stievenart, M.; Charistophe, J  
Biochem. Biophys. Res. Commun. 191, 479-486, 1993  
A;Title: Small introns in a hepatic cDNA encoding a new glucagon-like peptide 1-type re  
A;Reference number: JQ1957; MUID:93213282; PMID:8384842  
A;Accession: JQ1957  
A;Molecule type: mRNA  
A;Residues: 1-485 <SVO>  
A;Cross-references: UNIPROT:P30082; GB:X68692  
A;Experimental source: liver  
R;Jelinek, L.J.; Lok, S.; Rosenberg, G.B.; Smith, R.A.; Grant, F.J.; Biggs, S.; Bensch,  
rnan, P.A.; Kindsvogel, W.  
Science 259, 1614-1616, 1993  
A;Title: Expression cloning and signaling properties of the rat glucagon receptor.  
A;Reference number: A46211; MUID:93206096; PMID:8384375  
A;Accession: A46211  
A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tr  
A;Molecule type: mRNA  
A;Residues: 1-37, 'W', '38-215', 'W', '217-323', 'V', '325-485' <JEL>  
A;Experimental source: liver  
A;Note: sequence extracted from NCBI backbone (NCBIP:127785)  
C;Genetics:  
A;Introns: 132/3; 168/2; 220/3; 407/3  
C;Superfamily: glucagon receptor



C;Keywords: G protein-coupled receptor; glycoprotein; liver; phosphoprotein; transmembrane  
F;144-167/Domain: transmembrane #status predicted <TM1>  
F;175-194/Domain: transmembrane #status predicted <TM2>  
F;227-251/Domain: transmembrane #status predicted <TM3>  
F;264-286/Domain: transmembrane #status predicted <TM4>  
F;305-324/Domain: transmembrane #status predicted <TM5>  
F;352-370/Domain: transmembrane #status predicted <TM6>  
F;389-405/Domain: transmembrane #status predicted <TM7>  
F;47,60,75,79/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F;432/Binding site: phosphate (Ser) (covalent) #status predicted

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Best Local Similarity 100.0%; Pred. No. 20;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 42 VLSCLPK 48  
|||  
Db 17 VLSCLPK 23

## RESULT 15

S74561

hypothetical protein s110225 - Synechocystis sp. (strain PCC 6803)

C;Species: Synechocystis sp.

A;Variety: PCC 6803

C;Date: 25-Apr-1997 #sequence\_revision 25-Apr-1997 #text\_change 09-Jul-2004

C;Accession: S74561

R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;

O. K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda

DNA Res. 3, 109-136, 1996

A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis

S;Reference number: S74322; MUID:97061201; PMID:8905231

A;Accession: S74561

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-512 &lt;KAN&gt;

A;Cross-references: UNIPROT:P72706; EMBL:D90900; GB:AB001339; NID:g1651768; PIDN:BA1671

A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

C;Genetics:

A;Start codon: GTG

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Best Local Similarity 100.0%; Pred. No. 21;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 FLVPVPG 20  
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Db 424 FLVPVPG 430

Search completed: October 13, 2004, 15:01:12  
Job time : 41 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 13, 2004, 14:54:25 ; Search time 129 Seconds  
(without alignments)  
162.592 Million cell updates/sec

Title: US-10-272-121-2

Perfect score: 65  
Sequence: 1 MRIHYLLFALLFLVFPVG.....LPKEQIGKSTRGRKCCR 65

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 1356558 seqs, 322682953 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1356558

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

Published Applications\_AA:\*

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2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep:\*  
3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*  
4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep:\*  
5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep:\*  
6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep:\*  
7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep:\*  
8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*  
9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep:\*  
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11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep:\*  
12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep:\*  
13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep:\*  
14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep:\*  
15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep:\*  
16: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pep:\*  
17: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep:\*  
18: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\*  
19: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep:\*

Pred. NO. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	DB ID	Description
1	65	100.0	65	14	US-10-091-166B-2
2	65	100.0	65	14	US-10-272-121-2
3	65	100.0	65	14	US-10-409-366-2
4	65	100.0	65	14	US-10-409-532-2
5	65	100.0	67	9	US-09-917-340-52
6	65	100.0	67	9	US-09-917-340-72
7	65	100.0	67	9	US-09-872-852-2
8	65	100.0	67	14	US-10-091-166B-10
9	65	100.0	67	14	US-10-272-121-10
10	65	100.0	67	14	US-10-409-366-10
11	65	100.0	67	14	US-10-409-532-10
12	43	66.2	45	9	US-09-872-852-4
13	42	64.6	44	16	US-10-332-765-27
14	39	60.0	41	9	US-09-872-852-3

15	35	53.8	35	14	US-10-252-734-7	Sequence 7, Appli
16	31	47.7	31	16	US-10-332-765-1	Sequence 1, Appli
17	20	30.8	36	14	US-10-091-166B-60	Sequence 60, Appl
18	20	30.8	36	14	US-10-272-121-60	Sequence 60, Appl
19	20	30.8	36	14	US-10-409-366-60	Sequence 60, Appl
20	20	30.8	36	14	US-10-409-532-60	Sequence 60, Appl
21	20	30.8	37	14	US-10-091-166B-58	Sequence 58, Appl
22	20	30.8	37	14	US-10-091-166B-59	Sequence 58, Appl
23	20	30.8	37	14	US-10-272-121-58	Sequence 59, Appl
24	20	30.8	37	14	US-10-272-121-59	Sequence 59, Appl
25	20	30.8	37	14	US-10-409-366-58	Sequence 58, Appl
26	20	30.8	37	14	US-10-409-366-59	Sequence 59, Appl
27	20	30.8	37	14	US-10-409-532-58	Sequence 59, Appl
28	20	30.8	37	14	US-10-409-532-59	Sequence 59, Appl
29	20	30.8	38	14	US-10-091-166B-56	Sequence 56, Appl
30	20	30.8	38	14	US-10-091-166B-57	Sequence 56, Appl
31	20	30.8	38	14	US-10-272-121-56	Sequence 57, Appl
32	20	30.8	38	14	US-10-272-121-57	Sequence 57, Appl
33	20	30.8	38	14	US-10-409-366-56	Sequence 56, Appl
34	20	30.8	38	14	US-10-409-366-57	Sequence 56, Appl
35	20	30.8	38	14	US-10-409-532-56	Sequence 57, Appl
36	20	30.8	38	14	US-10-409-532-57	Sequence 57, Appl
37	20	30.8	39	14	US-10-091-166B-54	Sequence 54, Appl
38	20	30.8	39	14	US-10-091-166B-55	Sequence 54, Appl
39	20	30.8	39	14	US-10-272-121-54	Sequence 55, Appl
40	20	30.8	39	14	US-10-272-121-55	Sequence 55, Appl
41	20	30.8	39	14	US-10-409-366-54	Sequence 54, Appl
42	20	30.8	39	14	US-10-409-366-55	Sequence 54, Appl
43	20	30.8	39	14	US-10-409-532-54	Sequence 55, Appl
44	20	30.8	39	14	US-10-409-532-55	Sequence 55, Appl
45	20	30.8	40	14	US-10-091-166B-52	Sequence 52, Appl

ALIGNMENTS

RESULT 1

US-10-091-166B-2

Sequence 2, Appli

Publication No. US20030143671A1

GENERAL INFORMATION:

APPLICANT: Adler, David A.

APPLICANT: Holloway, James L.

APPLICANT: Bairdur, Nand

APPLICANT: Beigel-Orme, Stephanie

APPLICANT: Sheppard, Paul O.

TITLE OF INVENTION: NOVEL BETA-DEFENSINS

FILE REFERENCE: 97-44D1

CURRENT APPLICATION NUMBER: US/10/091,166B

CURRENT FILING DATE: 2002-03-05

PRIOR APPLICATION NUMBER: US 09/636,399

PRIOR FILING DATE: 2000-08-10

PRIOR APPLICATION NUMBER: US 09/344,097

PRIOR FILING DATE: 1999-06-25

PRIOR APPLICATION NUMBER: US 09/150,786

PRIOR FILING DATE: 1998-09-10

PRIOR APPLICATION NUMBER: US 60/064,294

PRIOR FILING DATE: 1997-11-05

PRIOR APPLICATION NUMBER: US 60/058,335

PRIOR FILING DATE: 1997-09-10

NUMBER OF SEQ ID NOS: 72

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 2

LENGTH: 65

TYPE: PRT

ORGANISM: Homo sapiens

US-10-091-166B-2

Query Match 100.0%; Score 65; DB 14; length 65;

Best Local Similarity 100.0%; Pred. No. 8.3e-59;

Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MRIHYLLFALLFLFLVPGHGGIINTLQKYYCRVGRCAVLSCLPKEQIGKCTRGR 60  
QY 61 KCCRR 65  
Db 61 KCCRR 65

RESULT 2  
US-10-272-121-2  
; Sequence 2, Application US/10272121  
; Publication No. US20030157638A1  
; GENERAL INFORMATION:  
; APPLICANT: Adler, David A.  
; APPLICANT: Holloway, James L.  
; APPLICANT: Bairdur, Nand  
; APPLICANT: Beigel-Orme, Stephanie  
; APPLICANT: Sheppard, Paul O.  
; TITLE OF INVENTION: NOVEL BETA-DEFENSINS  
; FILE REFERENCE: 97-44D2  
; CURRENT APPLICATION NUMBER: US/10/272,121  
; CURRENT FILING DATE: 2002-10-15  
; PRIOR APPLICATION NUMBER: US 09/636,399  
; PRIOR FILING DATE: 2000-08-10  
; PRIOR APPLICATION NUMBER: US 09/344,097  
; PRIOR FILING DATE: 1999-06-25  
; PRIOR APPLICATION NUMBER: US 09/150,786  
; PRIOR FILING DATE: 1998-09-10  
; PRIOR APPLICATION NUMBER: US 60/064,294  
; PRIOR FILING DATE: 1997-11-05  
; PRIOR APPLICATION NUMBER: US 60/058,335  
; PRIOR FILING DATE: 1997-09-10  
; NUMBER OF SEQ ID NOS: 72  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 65  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-272-121-2

Query Match 100.0%; Score 65; DB 14; Length 65;  
Best Local Similarity 100.0%; Pred. No. 8.3e-59;  
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 KCCRR 65  
Db 61 KCCRR 65

RESULT 3  
US-10-409-366-2  
; Sequence 2, Application US/10409366  
; Publication No. US20030166912A1  
; GENERAL INFORMATION:  
; APPLICANT: Adler, David A.  
; APPLICANT: Holloway, James L.  
; APPLICANT: Bairdur, Nand  
; APPLICANT: Beigel-Orme, Stephanie  
; APPLICANT: Sheppard, Paul O.  
; TITLE OF INVENTION: NOVEL BETA-DEFENSINS  
; FILE REFERENCE: 97-44C2  
; CURRENT APPLICATION NUMBER: US/10/409,366  
; CURRENT FILING DATE: 2003-04-07  
; PRIOR APPLICATION NUMBER: US/09/636,399A  
; PRIOR FILING DATE: 2000-08-10  
; PRIOR APPLICATION NUMBER: 60/058,335  
; PRIOR FILING DATE: 1997-10-09  
; PRIOR APPLICATION NUMBER: 60/064,294  
; PRIOR FILING DATE: 1997-11-05

; PRIOR APPLICATION NUMBER: 09/150,786  
; PRIOR FILING DATE: 1998-09-10  
; PRIOR APPLICATION NUMBER: 09/636,399  
; PRIOR FILING DATE: 2000-08-10  
; NUMBER OF SEQ ID NOS: 72  
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; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-409-366-2

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Best Local Similarity 100.0%; Pred. No. 8.3e-59;  
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QY 61 KCCRR 65  
Db 61 KCCRR 65

RESULT 4  
US-10-409-532-2  
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; Publication No. US20030166913A1  
; GENERAL INFORMATION:  
; APPLICANT: Adler, David A.  
; APPLICANT: Holloway, James L.  
; APPLICANT: Bairdur, Nand  
; APPLICANT: Beigel-Orme, Stephanie  
; APPLICANT: Sheppard, Paul O.  
; TITLE OF INVENTION: NOVEL BETA-DEFENSINS  
; FILE REFERENCE: 97-44C2  
; CURRENT APPLICATION NUMBER: US/10/409,532  
; CURRENT FILING DATE: 2003-04-07  
; PRIOR APPLICATION NUMBER: US/09/636,399A  
; PRIOR FILING DATE: 2000-08-10  
; PRIOR APPLICATION NUMBER: 60/058,335  
; PRIOR FILING DATE: 1997-10-09  
; PRIOR APPLICATION NUMBER: 60/064,294  
; PRIOR FILING DATE: 1997-11-05  
; PRIOR APPLICATION NUMBER: 09/150,786  
; PRIOR FILING DATE: 1998-09-10  
; PRIOR APPLICATION NUMBER: 09/636,399  
; PRIOR FILING DATE: 2000-08-10  
; NUMBER OF SEQ ID NOS: 72  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 2  
; LENGTH: 65  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-409-532-2

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Best Local Similarity 100.0%; Pred. No. 8.3e-59;  
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MRIHYLLFALLFLFLVPGHGGIINTLQKYYCRVGRCAVLSCLPKEQIGKCTRGR 60

QY 61 KCCRR 65  
Db 61 KCCRR 65

RESULT 5  
US-09-917-340-52  
; Sequence 52, Application US/09917340

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; Patent No: US20020090369A1
; GENERAL INFORMATION:
; APPLICANT: Murphy, Christopher J.
; APPLICANT: McAnulty, Jonathan F.
; APPLICANT: Reid, Ted W.
; TITLE OF INVENTION: Transplant Media
; FILE REFERENCE: TPLANT-06468
; CURRENT APPLICATION NUMBER: US/09/917,340
; CURRENT FILING DATE: 2001-07-29
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 60/249,602
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/290,932
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 52
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-917-340-52

Query Match          100.0%; Score 65; DB 9; Length 67;
Best Local Similarity 100.0%; Pred. No. 8.5e-59;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      61 KCCRR 65
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Db      61 KCCRR 65

RESULT 6
US-09-917-340-72
; Sequence 72, Application US/09917340
; Patent No. US20020090369A1
; GENERAL INFORMATION:
; APPLICANT: Murphy, Christopher J.
; APPLICANT: McAnulty, Jonathan F.
; APPLICANT: Reid, Ted W.
; TITLE OF INVENTION: Transplant Media
; FILE REFERENCE: TPLANT-06468
; CURRENT APPLICATION NUMBER: US/09/917,340
; CURRENT FILING DATE: 2001-07-29
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 60/221,632
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 60/249,602
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/290,932
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 72
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-917-340-72

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Best Local Similarity 100.0%; Pred. No. 8.5e-59;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      61 KCCRR 65
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Db      61 KCCRR 65
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RESULT 7
US-09-872-852-2
; Sequence 2, Application US/09872852
; Patent No. US20020115602A1
; GENERAL INFORMATION:
; APPLICANT: MCCRAY JR, PAUL B.
; APPLICANT: TACK, BRIAN
; APPLICANT: JIA, HONG PENG
; APPLICANT: SCHUTTE, BRIAN C.
; TITLE OF INVENTION: HUMAN BETA-DEFENSIN-3 (HBD-3), A HIGHLY CATIONIC
; FILE REFERENCE: IOWA.031US
; CURRENT APPLICATION NUMBER: US/09/872,852
; CURRENT FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: 60/208,792
; PRIOR FILING DATE: 2000-06-01
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; US-09-872-852-2

Query Match          100.0%; Score 65; DB 9; Length 67;
Best Local Similarity 100.0%; Pred. No. 8.5e-59;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MRIHYLLFALLFLVLPVPGHGIINTLQKYYCVRGRCVAVLSCLPKKEQIGKSTRGR 60
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Db      1 MRIHYLLFALLFLVLPVPGHGIINTLQKYYCVRGRCVAVLSCLPKKEQIGKSTRGR 60

QY      61 KCCRR 65
      |||
Db      61 KCCRR 65

RESULT 8
US-10-091-166B-10
; Sequence 10, Application US/10091166B
; Publication No. US20030143671A1
; GENERAL INFORMATION:
; APPLICANT: Adler, David A.
; APPLICANT: Holloway, James L.
; APPLICANT: Baidur, Nand
; APPLICANT: Beigel-Orme, Stephanie
; APPLICANT: Shepard, Paul O.
; TITLE OF INVENTION: NOVEL BETA-DEFENSINS
; FILE REFERENCE: 97-44D1
; CURRENT APPLICATION NUMBER: US/10/091,166B
; CURRENT FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 09/636,399
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: US 09/344,097
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 09/150,786
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: US 60/064,294
; PRIOR FILING DATE: 1997-11-05
; PRIOR APPLICATION NUMBER: US 60/058,335
; PRIOR FILING DATE: 1997-09-10
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-091-166B-10
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Query Match 100.0%; Score 65; DB 14; Length 67;  
Best Local Similarity 100.0%; Pred. No. 8.5e-59;  
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRIHYLLFALLFLVLPVPGHGGIINTLQKYYCVRVGGRCAYLSCLPKKEQIGKCTRGR 60  
DB 1 MRIHYLLFALLFLVLPVPGHGGIINTLQKYYCVRVGGRCAYLSCLPKKEQIGKCTRGR 60  
QY 61 KCCRR 65  
DB 61 KCCRR 65

RESULT 9  
US-10-272-121-10

; Sequence 10, Application US/10272121  
; Publication No. US20030157638A1  
; GENERAL INFORMATION:  
; APPLICANT: Adler, David A.  
; APPLICANT: Holloway, James L.  
; APPLICANT: Baindur, Nand  
; APPLICANT: Beigel-Orme, Stephanie  
; APPLICANT: Shepard, Paul O.  
; TITLE OF INVENTION: NOVEL BETA-DEFENSINS  
; FILE REFERENCE: 97-44D2  
; CURRENT APPLICATION NUMBER: US/10/272,121  
; PRIOR FILING DATE: 2002-10-15  
; PRIOR APPLICATION NUMBER: US 09/636,399  
; PRIOR FILING DATE: 2000-08-10  
; PRIOR APPLICATION NUMBER: US 09/344,097  
; PRIOR FILING DATE: 1999-06-25  
; PRIOR APPLICATION NUMBER: US 09/150,786  
; PRIOR FILING DATE: 1998-09-10  
; PRIOR APPLICATION NUMBER: US 60/064,294  
; PRIOR FILING DATE: 1997-11-05  
; PRIOR APPLICATION NUMBER: US 60/058,335  
; PRIOR FILING DATE: 1997-09-10  
; NUMBER OF SEQ ID NOS: 72  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 10  
; LENGTH: 67  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-272-121-10

Query Match 100.0%; Score 65; DB 14; Length 67;  
Best Local Similarity 100.0%; Pred. No. 8.5e-59;  
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRIHYLLFALLFLVLPVPGHGGIINTLQKYYCVRVGGRCAYLSCLPKKEQIGKCTRGR 60  
DB 1 MRIHYLLFALLFLVLPVPGHGGIINTLQKYYCVRVGGRCAYLSCLPKKEQIGKCTRGR 60  
QY 61 KCCRR 65  
DB 61 KCCRR 65

RESULT 10  
US-10-409-366-10

; Sequence 10, Application US/10409366  
; Publication No. US20030166912A1  
; GENERAL INFORMATION:  
; APPLICANT: Adler, David A.  
; APPLICANT: Holloway, James L.  
; APPLICANT: Baindur, Nand  
; APPLICANT: Beigel-Orme, Stephanie  
; APPLICANT: Shepard, Paul O.  
; TITLE OF INVENTION: NOVEL BETA-DEFENSINS  
; FILE REFERENCE: 97-44C2  
; CURRENT APPLICATION NUMBER: US/10/409,366  
; CURRENT FILING DATE: 2003-04-07

; PRIOR APPLICATION NUMBER: US/09/636,399A  
; PRIOR FILING DATE: 2000-08-10  
; PRIOR APPLICATION NUMBER: 60/058,335  
; PRIOR FILING DATE: 1997-10-09  
; PRIOR APPLICATION NUMBER: 60/064,294  
; PRIOR FILING DATE: 1997-11-05  
; PRIOR APPLICATION NUMBER: 09/150,786  
; PRIOR FILING DATE: 1998-09-10  
; PRIOR APPLICATION NUMBER: 09/636,399  
; PRIOR FILING DATE: 2000-08-10  
; NUMBER OF SEQ ID NOS: 72  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 10  
; LENGTH: 67  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-409-366-10

Query Match 100.0%; Score 65; DB 14; Length 67;  
Best Local Similarity 100.0%; Pred. No. 8.5e-59;  
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRIHYLLFALLFLVLPVPGHGGIINTLQKYYCVRVGGRCAYLSCLPKKEQIGKCTRGR 60  
DB 1 MRIHYLLFALLFLVLPVPGHGGIINTLQKYYCVRVGGRCAYLSCLPKKEQIGKCTRGR 60  
QY 61 KCCRR 65  
DB 61 KCCRR 65

RESULT 11  
US-10-409-532-10

; Sequence 10, Application US/10409532  
; Publication No. US20030166913A1  
; GENERAL INFORMATION:  
; APPLICANT: Adler, David A.  
; APPLICANT: Holloway, James L.  
; APPLICANT: Baindur, Nand  
; APPLICANT: Beigel-Orme, Stephanie  
; APPLICANT: Shepard, Paul O.  
; TITLE OF INVENTION: NOVEL BETA-DEFENSINS  
; FILE REFERENCE: 97-44C2  
; CURRENT APPLICATION NUMBER: US/10/409,532  
; CURRENT FILING DATE: 2003-04-07  
; PRIOR APPLICATION NUMBER: US/09/636,399A  
; PRIOR FILING DATE: 2000-08-10  
; PRIOR APPLICATION NUMBER: 60/058,335  
; PRIOR FILING DATE: 1997-10-09  
; PRIOR APPLICATION NUMBER: 60/064,294  
; PRIOR FILING DATE: 1997-11-05  
; PRIOR APPLICATION NUMBER: 09/150,786  
; PRIOR FILING DATE: 1998-09-10  
; PRIOR APPLICATION NUMBER: 09/636,399  
; PRIOR FILING DATE: 2000-08-10  
; NUMBER OF SEQ ID NOS: 72  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 10  
; LENGTH: 67  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-409-532-10

Query Match 100.0%; Score 65; DB 14; Length 67;  
Best Local Similarity 100.0%; Pred. No. 8.5e-59;  
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRIHYLLFALLFLVLPVPGHGGIINTLQKYYCVRVGGRCAYLSCLPKKEQIGKCTRGR 60  
DB 1 MRIHYLLFALLFLVLPVPGHGGIINTLQKYYCVRVGGRCAYLSCLPKKEQIGKCTRGR 60  
QY 61 KCCRR 65

Db 61 KCCR 65

## RESULT 12

US-09-872-852-4  
; Sequence 4, Application US/09872852  
; Patent No. US20020115602A1  
; GENERAL INFORMATION:  
; APPLICANT: MCCRAY JR, PAUL B.  
; APPLICANT: TACK, BRIAN  
; APPLICANT: JIA, HONG PENG  
; APPLICANT: SCHUTTE, BRIAN C.  
; TITLE OF INVENTION: HUMAN BETA-DEFENSIN-3 (HBD-3), A HIGHLY CATIONIC  
; FILE REFERENCE: IOWA:031US  
; CURRENT APPLICATION NUMBER: US/09/872,852  
; PRIOR FILING DATE: 2001-06-01  
; PRIOR FILING DATE: 2000-06-01  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: Patentln Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 45  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: Peptide  
US-09-872-852-4

Query Match 66.2%; Score 43; DB 9; Length 45;  
Best Local Similarity 100.0%; Pred. No. 2e-36;  
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 GIINTLQKYYCRVGRGRCVAVLSCLPKKEQIGKCGSTRGRKCCR 65

Db 1 GIINTLQKYYCRVGRGRCVAVLSCLPKKEQIGKCGSTRGRKCCR 43

## RESULT 13

US-10-332-765-27  
; Sequence 27, Application US/10332765  
; Publication No. US20040116652A1  
; GENERAL INFORMATION:  
; APPLICANT: Forsmann, Wolf-Georg  
; APPLICANT: Conejo-Garcia, Jose-Ramon  
; APPLICANT: Adermann, Knut  
; TITLE OF INVENTION: Method for Producing and Using Novel Human Defensins as Biologics  
; FILE REFERENCE: 022584us  
; CURRENT APPLICATION NUMBER: US/10/332,765  
; PRIOR FILING DATE: 2003-01-13  
; PRIOR FILING DATE: 2000-07-11  
; NUMBER OF SEQ ID NOS: 78  
; SOFTWARE: Patentln Ver. 2.1  
; SEQ ID NO 27  
; LENGTH: 44  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-332-765-27

Query Match 64.6%; Score 42; DB 16; Length 44;  
Best Local Similarity 100.0%; Pred. No. 2.1e-35;  
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 IINTLQKYYCRVGRGRCVAVLSCLPKKEQIGKCGSTRGRKCCR 65

Db 1 IINTLQKYYCRVGRGRCVAVLSCLPKKEQIGKCGSTRGRKCCR 42

RESULT 14  
US-09-872-852-3

; Sequence 3, Application US/09872852  
; Patent No. US20020115602A1  
; GENERAL INFORMATION:  
; APPLICANT: MCCRAY JR, PAUL B.  
; APPLICANT: TACK, BRIAN  
; APPLICANT: JIA, HONG PENG  
; APPLICANT: SCHUTTE, BRIAN C.  
; TITLE OF INVENTION: HUMAN BETA-DEFENSIN-3 (HBD-3), A HIGHLY CATIONIC  
; FILE REFERENCE: IOWA:031US  
; CURRENT APPLICATION NUMBER: US/09/872,852  
; PRIOR FILING DATE: 2001-06-01  
; PRIOR FILING DATE: 2000-06-01  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: Patentln Ver. 2.1  
; SEQ ID NO 3  
; LENGTH: 41  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: Peptide  
US-09-872-852-3

Query Match 60.0%; Score 39; DB 9; Length 41;  
Best Local Similarity 100.0%; Pred. No. 2.3e-32;  
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 TLQKYYCRVGRGRCVAVLSCLPKKEQIGKCGSTRGRKCCR 65

Db 1 TLQKYYCRVGRGRCVAVLSCLPKKEQIGKCGSTRGRKCCR 39

## RESULT 15

US-10-252-734-7  
; Sequence 7, Application US/10252734  
; Publication No. US20030176652A1  
; GENERAL INFORMATION:  
; APPLICANT: MCCRAY, JR., PAUL B.  
; APPLICANT: SCHUTTE, BRIAN C.  
; APPLICANT: JIA, HONG PENG  
; APPLICANT: CASAVANT, THOMAS L.  
; TITLE OF INVENTION: HUMAN AND MOUSE b-DEFENSINS, ANTIMICROBIAL PEPTIDES  
; FILE REFERENCE: IOWA:041US  
; CURRENT APPLICATION NUMBER: US/10/252,734  
; PRIOR FILING DATE: 2002-09-23  
; PRIOR FILING DATE: 2001-09-21  
; NUMBER OF SEQ ID NOS: 82  
; SOFTWARE: Patentln Ver. 2.1  
; SEQ ID NO 7  
; LENGTH: 35  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-252-734-7

Query Match 53.8%; Score 35; DB 14; Length 35;  
Best Local Similarity 100.0%; Pred. No. 2.5e-28;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 YYCRVGRGRCVAVLSCLPKKEQIGKCGSTRGRKCCR 65

Db 1 YYCRVGRGRCVAVLSCLPKKEQIGKCGSTRGRKCCR 35

Search completed: October 13, 2004, 15:04:09  
Job time : 130 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 13, 2004, 14:52:15 ; Search time 38 Seconds  
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Title: US-10-272-121-2

Perfect score: 65  
Sequence: 1 MRLHYLLFALLFLFLVPPVG.....LPKEEQIGKCKSTRGRKCCRR 65

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Gapop 60.0 , Gapext 60.0

Searched: 478139 seqs, 66318000 residues

Word size : 0

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0  
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Post-processing: Listing first 45 summaries

Database : Issued Patents AA: \*  
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2: /cgn2\_6/ptodata/1/iaa/5B.COMB.pep: \*  
3: /cgn2\_6/ptodata/1/iaa/6A.COMB.pep: \*  
4: /cgn2\_6/ptodata/1/iaa/6B.COMB.pep: \*  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	65	100.0	65	4	US-09-636-399A-2
2	65	100.0	67	4	US-09-636-399A-10
3	65	100.0	67	4	US-09-917-340-52
4	65	100.0	67	4	US-09-917-340-72
5	20	30.8	36	4	US-09-636-399A-60
6	20	30.8	37	4	US-09-636-399A-58
7	20	30.8	37	4	US-09-636-399A-59
8	20	30.8	38	4	US-09-636-399A-56
9	20	30.8	38	4	US-09-636-399A-57
10	20	30.8	39	4	US-09-636-399A-54
11	20	30.8	39	4	US-09-636-399A-55
12	20	30.8	40	4	US-09-636-399A-52
13	20	30.8	40	4	US-09-636-399A-53
14	20	30.8	41	4	US-09-636-399A-50
15	20	30.8	41	4	US-09-636-399A-51
16	20	30.8	42	4	US-09-636-399A-48
17	20	30.8	42	4	US-09-636-399A-49
18	20	30.8	43	4	US-09-636-399A-46
19	20	30.8	43	4	US-09-636-399A-47
20	20	30.8	44	4	US-09-636-399A-44
21	20	30.8	44	4	US-09-636-399A-45
22	20	30.8	45	4	US-09-636-399A-42
23	20	30.8	45	4	US-09-636-399A-43
24	20	30.8	46	4	US-09-636-399A-40
25	20	30.8	46	4	US-09-636-399A-41
26	20	30.8	47	4	US-09-636-399A-38
27	20	30.8	47	4	US-09-636-399A-39

28	20	30.8	48	4	US-09-636-399A-36	Sequence 36, Appl
29	20	30.8	48	4	US-09-636-399A-37	Sequence 37, Appl
30	20	30.8	49	4	US-09-636-399A-35	Sequence 35, Appl
31	19	29.2	35	4	US-09-636-399A-62	Sequence 62, Appl
32	19	29.2	36	4	US-09-636-399A-61	Sequence 61, Appl
33	18	27.7	34	4	US-09-636-399A-64	Sequence 64, Appl
34	18	27.7	35	4	US-09-636-399A-63	Sequence 63, Appl
35	17	26.2	33	4	US-09-636-399A-66	Sequence 66, Appl
36	17	26.2	34	4	US-09-636-399A-65	Sequence 65, Appl
37	16	24.6	32	4	US-09-636-399A-68	Sequence 68, Appl
38	16	24.6	33	4	US-09-636-399A-67	Sequence 67, Appl
39	15	23.1	31	4	US-09-636-399A-70	Sequence 70, Appl
40	15	23.1	32	4	US-09-636-399A-69	Sequence 69, Appl
41	14	21.5	30	4	US-09-636-399A-72	Sequence 72, Appl
42	14	21.5	31	4	US-09-636-399A-71	Sequence 71, Appl
43	14	21.5	37	4	US-09-636-399A-14	Sequence 14, Appl
44	14	21.5	38	4	US-09-636-399A-18	Sequence 18, Appl
45	14	21.5	38	4	US-09-636-399A-34	Sequence 34, Appl

ALIGNMENTS

RESULT 1  
US-09-636-399A-2  
; Sequence 2, Application US/09636399A  
; Patent No. 6576755  
; GENERAL INFORMATION:  
; APPLICANT: Adler, David A.  
; APPLICANT: Holloway, James L.  
; APPLICANT: Balindur, Nand  
; APPLICANT: Beigel-Orme, Stephanie  
; APPLICANT: Sheppard, Paul O.  
; TITLE OF INVENTION: NOVEL BETA-DEFENSINS  
; FILE REFERENCE: 97-44C2  
; CURRENT APPLICATION NUMBER: US/09/636,399A  
; CURRENT FILING DATE: 2000-08-10  
; PRIOR APPLICATION NUMBER: 60/058,335  
; PRIOR FILING DATE: 1997-10-09  
; PRIOR APPLICATION NUMBER: 60/064,294  
; PRIOR FILING DATE: 1997-11-05  
; PRIOR APPLICATION NUMBER: 09/150,786  
; PRIOR FILING DATE: 1998-09-10  
; PRIOR APPLICATION NUMBER: 09/636,399  
; PRIOR FILING DATE: 2000-08-10  
; NUMBER OF SEQ ID NOS: 72  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 2  
; LENGTH: 65  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-09-636-399A-2  
Query Match 100.0%; Score 65; DB 4; Length 65;  
Best Local Similarity 100.0%; Pred. No. 2.9e-63;  
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MRLHYLLFALLFLFLVPPVGHGIIINTLQKYYCRVGRCAVLSCLPKKEQIGKCKSTRGR 60  
DB 1 MRLHYLLFALLFLFLVPPVGHGIIINTLQKYYCRVGRCAVLSCLPKKEQIGKCKSTRGR 60  
QY 61 KCCRR 65  
DB 61 KCCRR 65  
RESULT 2  
US-09-636-399A-10  
; Sequence 10, Application US/09636399A  
; Patent No. 6576755  
; GENERAL INFORMATION:  
; APPLICANT: Adler, David A.  
; APPLICANT: Holloway, James L.

```
APPLICANT: Baindur, Nand
APPLICANT: Beigel-Orme, Stephanie
APPLICANT: Sheppard, Paul O.
TITLE OF INVENTION: NOVEL BETA-DEFENSINS
FILE REFERENCE: 97-44C2
CURRENT APPLICATION NUMBER: US/09/636,399A
CURRENT FILING DATE: 2000-08-10
PRIOR APPLICATION NUMBER: 60/058,335
PRIOR FILING DATE: 1997-10-09
PRIOR APPLICATION NUMBER: 60/064,294
PRIOR FILING DATE: 1997-11-05
PRIOR APPLICATION NUMBER: 09/150,786
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 09/636,399
PRIOR FILING DATE: 2000-08-10
NUMBER OF SEQ ID NOS: 72
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 10
LENGTH: 67
TYPE: PRT
ORGANISM: Homo sapiens
US-09-636-399A-10
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Query Match      100.0%; Score 65; DB 4; Length 67;
Best Local Similarity 100.0%; Pred. No. 3e-63;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 MRLHYLLFALLFLFLVPVPGHGIINTLQKYYCVRVGRCAVLSCLPKEEQIGKSTRGR 60
DB 1 MRLHYLLFALLFLFLVPVPGHGIINTLQKYYCVRVGRCAVLSCLPKEEQIGKSTRGR 60
QY 61 KCCRR 65
DB 61 KCCRR 65
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## RESULT 3

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US-09-917-340-52
Sequence 52, Application US/09917340
Patent No. 6696238
GENERAL INFORMATION:
APPLICANT: Murphy, Christopher J.
APPLICANT: McNulty, Jonathan F.
APPLICANT: Reid, Ted W.
TITLE OF INVENTION: Transplant Media
FILE REFERENCE: TPLANT-06468
CURRENT APPLICATION NUMBER: US/09/917,340
CURRENT FILING DATE: 2001-07-29
PRIOR APPLICATION NUMBER: 60/221,632
PRIOR FILING DATE: 2000-07-28
PRIOR APPLICATION NUMBER: 60/249,602
PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/290,932
PRIOR FILING DATE: 2001-05-15
NUMBER OF SEQ ID NOS: 96
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 52
LENGTH: 67
TYPE: PRT
ORGANISM: Homo sapiens
US-09-917-340-52
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Query Match      100.0%; Score 65; DB 4; Length 67;
Best Local Similarity 100.0%; Pred. No. 3e-63;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 MRLHYLLFALLFLFLVPVPGHGIINTLQKYYCVRVGRCAVLSCLPKEEQIGKSTRGR 60
QY 61 KCCRR 65
DB 61 KCCRR 65
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RESULT 4
US-09-917-340-72
Sequence 72, Application US/09917340
Patent No. 6696238
GENERAL INFORMATION:
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APPLICANT: Murphy, Christopher J.
APPLICANT: McNulty, Jonathan F.
APPLICANT: Reid, Ted W.
TITLE OF INVENTION: Transplant Media
FILE REFERENCE: TPLANT-06468
CURRENT APPLICATION NUMBER: US/09/917,340
CURRENT FILING DATE: 2001-07-29
PRIOR APPLICATION NUMBER: 60/221,632
PRIOR FILING DATE: 2000-07-28
PRIOR APPLICATION NUMBER: 60/249,602
PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/290,932
PRIOR FILING DATE: 2001-05-15
NUMBER OF SEQ ID NOS: 96
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 72
LENGTH: 67
TYPE: PRT
ORGANISM: Homo sapiens
US-09-917-340-72
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Query Match      100.0%; Score 65; DB 4; Length 67;
Best Local Similarity 100.0%; Pred. No. 3e-63;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 MRLHYLLFALLFLFLVPVPGHGIINTLQKYYCVRVGRCAVLSCLPKEEQIGKSTRGR 60
DB 1 MRLHYLLFALLFLFLVPVPGHGIINTLQKYYCVRVGRCAVLSCLPKEEQIGKSTRGR 60
QY 61 KCCRR 65
DB 61 KCCRR 65
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## RESULT 5

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US-09-636-399A-60
Sequence 60, Application US/09636399A
Patent No. 6576755
GENERAL INFORMATION:
APPLICANT: Adler, David A.
APPLICANT: Holloway, James L.
APPLICANT: Baindur, Nand
APPLICANT: Beigel-Orme, Stephanie
APPLICANT: Sheppard, Paul O.
TITLE OF INVENTION: NOVEL BETA-DEFENSINS
FILE REFERENCE: 97-44C2
CURRENT APPLICATION NUMBER: US/09/636,399A
CURRENT FILING DATE: 2000-08-10
PRIOR APPLICATION NUMBER: 60/058,335
PRIOR FILING DATE: 1997-10-09
PRIOR APPLICATION NUMBER: 60/064,294
PRIOR FILING DATE: 1997-11-05
PRIOR APPLICATION NUMBER: 09/150,786
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 09/636,399
PRIOR FILING DATE: 2000-08-10
NUMBER OF SEQ ID NOS: 72
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 60
LENGTH: 36
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Defensin polypeptide
NAME/KEY: VARIANT
LOCATION: (33)...(33)
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; Sequence 57, Application US/09636399A
; Patent No. 6576755
; GENERAL INFORMATION:
; APPLICANT: Adler, David A.
; APPLICANT: Holloway, James L.
; APPLICANT: Baindur, Nand
; APPLICANT: Beigel-Orme, Stephanie
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: NOVEL BETA-DEFENSINS
; FILE REFERENCE: 97-44C2
; CURRENT APPLICATION NUMBER: US/09/636,399A
; CURRENT FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 60/058,335
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/064,294
; PRIOR FILING DATE: 1997-11-05
; PRIOR APPLICATION NUMBER: 09/150,786
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 09/636,399
; PRIOR FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 57
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Defensin polypeptide
; NAME/KEY: VARIANT
; LOCATION: (34)...(34)
; OTHER INFORMATION: Xaa is Ile, Leu, Val, Phe, or Met
US-09-636-399A-57

Query Match          30.8%; Score 20; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 1.4e-14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      31 YYCRVRRGRCVAVLSCLPKKE 50
Db      2 YYCRVRRGRCVAVLSCLPKKE 21

RESULT 10
US-09-636-399A-54
; Sequence 54, Application US/09636399A
; Patent No. 6576755
; GENERAL INFORMATION:
; APPLICANT: Adler, David A.
; APPLICANT: Holloway, James L.
; APPLICANT: Baindur, Nand
; APPLICANT: Beigel-Orme, Stephanie
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: NOVEL BETA-DEFENSINS
; FILE REFERENCE: 97-44C2
; CURRENT APPLICATION NUMBER: US/09/636,399A
; CURRENT FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 60/058,335
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/064,294
; PRIOR FILING DATE: 1997-11-05
; PRIOR APPLICATION NUMBER: 09/150,786
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 09/636,399
; PRIOR FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 54
; LENGTH: 39
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Defensin polypeptide
; NAME/KEY: VARIANT
; LOCATION: (34)...(34)
; OTHER INFORMATION: Xaa is Ile, Leu, Val, Phe, or Met
US-09-636-399A-54
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; LOCATION: (36)...(36)
; OTHER INFORMATION: Xaa is Leu, Ile, Met, Phe, or Val
US-09-636-399A-54

Query Match          30.8%; Score 20; DB 4; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.4e-14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      31 YYCRVRRGRCVAVLSCLPKKE 50
Db      4 YYCRVRRGRCVAVLSCLPKKE 23

RESULT 11
US-09-636-399A-55
; Sequence 55, Application US/09636399A
; Patent No. 6576755
; GENERAL INFORMATION:
; APPLICANT: Adler, David A.
; APPLICANT: Holloway, James L.
; APPLICANT: Baindur, Nand
; APPLICANT: Beigel-Orme, Stephanie
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: NOVEL BETA-DEFENSINS
; FILE REFERENCE: 97-44C2
; CURRENT APPLICATION NUMBER: US/09/636,399A
; CURRENT FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 60/058,335
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/064,294
; PRIOR FILING DATE: 1997-11-05
; PRIOR APPLICATION NUMBER: 09/150,786
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 09/636,399
; PRIOR FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 55
; LENGTH: 39
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Defensin polypeptide
; NAME/KEY: VARIANT
; LOCATION: (35)...(35)
; OTHER INFORMATION: Xaa is Leu, Val, Ile, Met, or Phe
US-09-636-399A-55

Query Match          30.8%; Score 20; DB 4; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.4e-14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      31 YYCRVRRGRCVAVLSCLPKKE 50
Db      3 YYCRVRRGRCVAVLSCLPKKE 22

RESULT 12
US-09-636-399A-52
; Sequence 52, Application US/09636399A
; Patent No. 6576755
; GENERAL INFORMATION:
; APPLICANT: Adler, David A.
; APPLICANT: Holloway, James L.
; APPLICANT: Baindur, Nand
; APPLICANT: Beigel-Orme, Stephanie
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: NOVEL BETA-DEFENSINS
; FILE REFERENCE: 97-44C2
; CURRENT APPLICATION NUMBER: US/09/636,399A
; CURRENT FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 60/058,335
; PRIOR FILING DATE: 1997-10-09
```

PRIOR APPLICATION NUMBER: 60/064,294  
PRIOR FILING DATE: 1997-11-05  
PRIOR APPLICATION NUMBER: 09/150,786  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 09/636,399  
PRIOR FILING DATE: 2000-08-10  
NUMBER OF SEQ ID NOS: 72  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 52  
LENGTH: 40  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Defensin polypeptide  
NAME/KEY: VARIANT  
LOCATION: (37)...(37)  
OTHER INFORMATION: Xaa is Met, Leu, Ile, Val, or Phe  
US-09-636-399A-52

Query Match 30.8%; Score 20; DB 4; Length 40;  
Best Local Similarity 100.0%; Pred. No. 1.4e-14;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 YYCRVRRGRCAYLSCLPKKE 50  
DB 5 YYCRVRRGRCAYLSCLPKKE 24

RESULT 13  
US-09-636-399A-53  
Sequence 53, Application US/09636399A  
Patent No. 6576755  
GENERAL INFORMATION:  
APPLICANT: Adler, David A.  
APPLICANT: Holloway, James L.  
APPLICANT: Baidur, Nand  
APPLICANT: Beigel-Orme, Stephanie  
APPLICANT: Sheppard, Paul O.  
TITLE OF INVENTION: NOVEL BETA-DEFENSINS  
FILE REFERENCE: 97-44C2  
CURRENT APPLICATION NUMBER: US/09/636,399A  
CURRENT FILING DATE: 2000-08-10  
PRIOR APPLICATION NUMBER: 60/058,335  
PRIOR FILING DATE: 1997-10-09  
PRIOR APPLICATION NUMBER: 60/064,294  
PRIOR FILING DATE: 1997-11-05  
PRIOR APPLICATION NUMBER: 09/150,786  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 09/636,399  
PRIOR FILING DATE: 2000-08-10  
NUMBER OF SEQ ID NOS: 72  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 53  
LENGTH: 40  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Defensin polypeptide  
NAME/KEY: VARIANT  
LOCATION: (36)...(36)  
OTHER INFORMATION: Xaa is Ile, Leu, Phe, Val, or Met  
US-09-636-399A-53

Query Match 30.8%; Score 20; DB 4; Length 40;  
Best Local Similarity 100.0%; Pred. No. 1.4e-14;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 YYCRVRRGRCAYLSCLPKKE 50  
DB 4 YYCRVRRGRCAYLSCLPKKE 23

RESULT 14

US-09-636-399A-50

Sequence 50, Application US/09636399A  
Patent No. 6576755  
GENERAL INFORMATION:  
APPLICANT: Adler, David A.  
APPLICANT: Holloway, James L.  
APPLICANT: Baidur, Nand  
APPLICANT: Beigel-Orme, Stephanie  
APPLICANT: Sheppard, Paul O.  
TITLE OF INVENTION: NOVEL BETA-DEFENSINS  
FILE REFERENCE: 97-44C2  
CURRENT APPLICATION NUMBER: US/09/636,399A  
CURRENT FILING DATE: 2000-08-10  
PRIOR APPLICATION NUMBER: 60/058,335  
PRIOR FILING DATE: 1997-10-09  
PRIOR APPLICATION NUMBER: 60/064,294  
PRIOR FILING DATE: 1997-11-05  
PRIOR APPLICATION NUMBER: 09/150,786  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 09/636,399  
PRIOR FILING DATE: 2000-08-10  
NUMBER OF SEQ ID NOS: 72  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 50  
LENGTH: 41  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Defensin polypeptide  
NAME/KEY: VARIANT  
LOCATION: (38)...(38)  
OTHER INFORMATION: Xaa is Ile, Leu, Phe, Val, or Met  
US-09-636-399A-50

Query Match 30.8%; Score 20; DB 4; Length 41;  
Best Local Similarity 100.0%; Pred. No. 1.5e-14;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 YYCRVRRGRCAYLSCLPKKE 50  
DB 6 YYCRVRRGRCAYLSCLPKKE 25

RESULT 15  
US-09-636-399A-51  
Sequence 51, Application US/09636399A  
Patent No. 6576755  
GENERAL INFORMATION:  
APPLICANT: Adler, David A.  
APPLICANT: Holloway, James L.  
APPLICANT: Baidur, Nand  
APPLICANT: Beigel-Orme, Stephanie  
APPLICANT: Sheppard, Paul O.  
TITLE OF INVENTION: NOVEL BETA-DEFENSINS  
FILE REFERENCE: 97-44C2  
CURRENT APPLICATION NUMBER: US/09/636,399A  
CURRENT FILING DATE: 2000-08-10  
PRIOR APPLICATION NUMBER: 60/058,335  
PRIOR FILING DATE: 1997-10-09  
PRIOR APPLICATION NUMBER: 60/064,294  
PRIOR FILING DATE: 1997-11-05  
PRIOR APPLICATION NUMBER: 09/150,786  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 09/636,399  
PRIOR FILING DATE: 2000-08-10  
NUMBER OF SEQ ID NOS: 72  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 51  
LENGTH: 41  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Defensin polypeptide

QY 31 YYCRVRRGRCAYLSCLPKKE 50  
DB 6 YYCRVRRGRCAYLSCLPKKE 25

; NAME/KEY: VARIANT  
; LOCATION: (37)...(37)  
; OTHER INFORMATION: Xaa is Ile, Leu, Phe, Val, or Met  
US-09-636-399A-51

Query Match 30.8%; Score 20; DB 4; Length 41;  
Best Local Similarity 100.0%; Pred. No. 1.5e-14;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 31 YYCRYRGRCAYLSCLPKKE 50  
|||  
Db 5 YYCRYRGRCAYLSCLPKKE 24

Search completed: October 13, 2004, 15:01:54  
Job time : 38 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 13, 2004, 14:47:19 ; Search time 158 Seconds  
(without alignments)  
147.579 Million cell updates/sec

Title: US-10-272-121-2  
Perfect score: 65  
Sequence: 1. MRLHYLLFALLFLFLVPPG.....LPXHEQIGKSTRGRKCCR 65

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 2002273 seqs, 358729299 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : A\_Geneseq\_23Sep04:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	65	100.0	65	2	AAV07243 Beta-defe
2	65	100.0	67	2	AAV07244 Beta-defe
3	65	100.0	67	3	AAAB10602 Human SAP
4	65	100.0	67	5	AAU09707 Human bet
5	65	100.0	67	5	AAU91016 Transplan
6	65	100.0	67	5	AAU91036 Transplan
7	65	100.0	67	8	AAO17768 Human bet
8	65	100.0	67	8	ADN05995 Antipsori
9	65	100.0	67	8	ADQ08006 Human bet
10	43	66.2	45	3	AAAB10600 Human SAP
11	43	66.2	45	5	AAU09709 Human bet
12	43	66.2	45	5	AAO17767 Human bet
13	39	60.0	41	5	AAU09708 Human bet
14	38	58.5	40	5	AAO17766 Human bet
15	35	53.8	35	6	ABR43502 Human bet
16	35	53.8	37	6	ABR43580 Human bet
17	32	49.2	32	3	AAAB10621 Human SAP
18	31	47.7	31	5	AAAM49576 Human bet
19	31	47.7	31	5	AAAM49572 Human bet
20	31	47.7	31	5	AAO17765 Human bet
21	31	47.7	51	2	AAI12039 Human 5'
22	27	41.5	40	7	ADG25620 Human hBD
23	25	38.5	27	5	AAO17781 Human bet
24	25	38.5	27	5	AAO17773 Human bet
25	22	33.8	22	5	AAO17772 Human bet

26	22	33.8	24	5	AAO17774	AAO17774 Human bet
27	19	29.2	19	5	AAO17770	AAO17770 Human bet
28	17	26.2	17	5	AAO17771	AAO17771 Human bet
29	17	26.2	17	5	AAO17780	AAO17780 Human bet
30	9	13.8	9	5	AAAM49573	AAAM49573 Human bet
31	9	13.8	63	4	AAE02126	AAE02126 Mouse bet
32	9	13.8	63	4	AAE02122	AAE02122 Mouse zam
33	8	12.3	63	4	AAO17769	AAO17769 Human bet
34	8	12.3	35	6	ABR43503	ABR43503 Mouse bet
35	8	12.3	63	4	AAE02127	AAE02127 Mouse bet
36	7	10.8	86	4	ABG29228	ABG29228 Novel hum
37	7	10.8	99	6	ABO15026	ABO15026 Human NOV
38	7	10.8	106	3	AAAB24085	AAAB24085 Human PRO
39	7	10.8	125	3	AAAB24086	AAAB24086 Human PRO
40	7	10.8	125	4	AAAB50995	AAAB50995 Human PRO
41	7	10.8	125	8	ADI03911	ADI03911 Human oxy
42	7	10.8	203	7	ADE55548	ADE55548 Rat Prote
43	7	10.8	219	7	ADD48307	ADD48307 Rat Prote
44	7	10.8	219	7	ADD48311	ADD48311 Rat Prote
45	7	10.8	229	4	ABG20028	ABG20028 Novel hum

ALIGNMENTS

RESULT 1.  
AAV07243  
ID AAV07243 standard, protein; 65 AA.  
XX  
AC AAV07243;  
XX  
DT 06-JUL-1999 (first entry)  
XX  
DE Beta-defensin family member zamp1.  
XX  
KW Human; zamp1; beta-defensin; bacterium; fungus; virus; inflammation;  
KW tissue damage; immune response; AIDS; chemotherapy; melanocortin;  
KW antibody; ion flux; cytotoxic activity; mammalian cell.  
XX  
OS Homo sapiens.  
XX  
PN WO9913080-A1.  
XX  
PD 18-MAR-1999.  
XX  
PF 10-SEP-1998; 98WO-US019222.  
XX  
PR 10-SEP-1997; 97US-0058335P.  
PR 10-SEP-1997; 97US-00926529.  
PR 05-NOV-1997; 97US-0064294P.  
PR 05-NOV-1997; 97US-00964687.  
XX  
PA (ZYMO ) ZYMOGENETICS INC.  
XX  
PI Adler D, Holloway JL, Bairdur N, Beigel S;  
XX  
DR WPI: 1999-215064/18.  
DR N-PSDB; AAX29985.  
XX  
PT New zamp1 polypeptide and polynucleotide, human beta-defensins - useful  
PT as diagnostic reagents and for treatment of microbial infections, and  
PT AIDS.  
XX  
PS Claim 1; Page 70; 79pp; English.  
XX  
CC This sequence represents the human zamp1 protein which is a member of the  
CC beta-defensin protein family. Zamp1 protein is useful as a pharmaceutical  
CC composition, useful for treatment of e.g. bacterial, fungal and viral  
CC infections. They are also useful pro-inflammatory, for treating chronic  
CC tissue damage, and for stimulating the immune response, for treatment of  
CC AIDS or chemotherapy patients. Zamp1 polypeptides and antibodies are  
CC useful for studying activity of the melanocortin family, studying ion  
CC flux in cell culture, and studying cytotoxic activity against mammalian

CC cells in culture, by incubation with the cells. Zamp1 polypeptides are  
CC especially useful for studying epithelial defensin induction in cell  
CC culture when exposed to pathogenic stimuli

XX Sequence 65 AA;

Query Match 100.0%; Score 65; DB 2; Length 65;

Best Local Similarity 100.0%; Pred. No. 1.8e-60;  
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRIHYLLFALLFLFVVPVPGHGIINTLQKYCRVRGRCVAVLSCLPKKEQIGKSTRGR 60  
DB 1 MRIHYLLFALLFLFVVPVPGHGIINTLQKYCRVRGRCVAVLSCLPKKEQIGKSTRGR 60

QY 61 KCCRR 65  
DB 61 KCCRR 65

RESULT 2  
AAY07244  
ID AAY07244 standard; protein; 67 AA.

AC AAY07244;  
XX  
DT 06-JUL-1999 (first entry)  
XX  
DE Beta-defensin family member zamp1.

XX Human; zamp1; beta-defensin; bacterium; fungus; virus; inflammation;  
KW tissue damage; immune response; AIDS; chemotherapy; melanocortin;  
KW antibody; ion flux; cytotoxic activity; mammalian cell.

OS Homo sapiens.

XX WO9913080-A1.

XX 18-MAR-1999.

XX 10-SEP-1998; 98WO-US019222.

XX 10-SEP-1997; 97US-0058335P.

XX 10-SEP-1997; 97US-00926529.

XX 05-NOV-1997; 97US-0064294P.

XX 05-NOV-1997; 97US-00964687.

XX (ZYMO ) ZYMOGENETICS INC.

XX Adler D, Holloway JL, Baidur N, Beigel S;

XX WPI: 1999-215064/18.

XX N-PSDB; AAX29986.

XX New zamp1 polypeptide and polynucleotide, human beta-defensins - useful  
XX as diagnostic reagents and for treatment of microbial infections, and  
XX AIDS.

XX Claim 1; Page 73; 79pp; English.

XX This sequence represents the human zamp1 protein which is a member of the  
XX beta-defensin protein family. Zamp1 protein is useful as a pharmaceutical  
XX composition, useful for treatment of e.g. bacterial, fungal and viral  
XX infections. They are also useful pro-inflammators, for treating chronic  
XX tissue damage, and for stimulating the immune response, for treatment of  
XX AIDS or chemotherapy patients. Zamp1 polypeptides and antibodies are  
XX useful for studying activity of the melanocortin family, studying ion  
XX flux in cell culture, and studying cytotoxic activity against mammalian  
XX cells in culture, by incubation with the cells. Zamp1 polypeptides are  
XX especially useful for studying epithelial defensin induction in cell  
XX culture when exposed to pathogenic stimuli

XX Sequence 67 AA;

Query Match 100.0%; Score 65; DB 2; Length 67;  
Best Local Similarity 100.0%; Pred. No. 1.9e-60;  
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRIHYLLFALLFLFVVPVPGHGIINTLQKYCRVRGRCVAVLSCLPKKEQIGKSTRGR 60  
DB 1 MRIHYLLFALLFLFVVPVPGHGIINTLQKYCRVRGRCVAVLSCLPKKEQIGKSTRGR 60

QY 61 KCCRR 65  
DB 61 KCCRR 65

RESULT 3  
AAB10602  
ID AAB10602 standard; protein; 67 AA.

AC AAB10602;  
XX  
DT 08-JAN-2001 (first entry)  
XX  
DE Human SAP-3 pre-protein.

XX SAP-2; SAP-3; human; antibiotic; antibacterial; antifungal; antiviral;  
KW treatment; microbial infection; wound dressing; diagnostic reagent.

OS Homo sapiens.

XX WO200046245-A2.

XX 10-AUG-2000.

XX 01-FEB-2000; 2000WO-EP000776.

XX 01-FEB-1999; 99DE-01005128.

XX 08-OCT-1999; 99DE-01049436.

XX (SCHD ) SCHERING AG.

XX Christophers E, Harder J, Schroeder J;

XX WPI: 2000-514948/46.

XX N-PSDB; AAA71755.

XX New human antibiotic peptides, useful for treating microbial infections,  
XX particularly when incorporated in wound dressings, also related nucleic  
XX acid.

XX Claim 4; Page 39; 41pp; German.

XX This invention describes the novel active, mature human proteins (I) SAP-  
XX 2 and SAP-3 which have antibiotic, antibacterial, antifungal and  
XX antiviral activity. (I), and their precursors, are useful for treating or  
XX preventing microbial infections (caused by bacteria, fungi or viruses),  
XX particularly where they (or human cells expressing them) are included in  
XX wound dressings, and to produce specific antibodies (Ab) or their  
XX fragments. Ab are used as diagnostic reagents, e.g. to detect a  
XX deficiency of (I) or the presence of a (I) variant. This sequence  
XX represents the human SAP-3 protein described in the method of the  
XX invention

XX Sequence 67 AA;

XX Query Match 100.0%; Score 65; DB 3; Length 67;

Best Local Similarity 100.0%; Pred. No. 1.9e-60;  
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRIHYLLFALLFLFVVPVPGHGIINTLQKYCRVRGRCVAVLSCLPKKEQIGKSTRGR 60  
DB 1 MRIHYLLFALLFLFVVPVPGHGIINTLQKYCRVRGRCVAVLSCLPKKEQIGKSTRGR 60

QY 61 KCCRR 65  
DB 61 KCCRR 65

Db 61 KCCRR 65

RESULT 4

AAU09707

ID AAU09707 standard; protein; 67 AA.

AC AAU09707;

DT 26-MAR-2002 (first entry)

DE Human beta-defensin-3 (HBD-3).

KW Human; antimicrobial peptide; human beta-defensin-3; HBD-3;

KM microbial growth; microbial infection; pulmonary infection.

OS Homo sapiens.

PN WO200192309-A2.

PD 06-DEC-2001.

PF 01-JUN-2001; 2001WO-US018057.

PR 01-JUN-2000; 2000US-0208792P.

PA (IOWA ) UNIV IOWA RES FOUND.

PI Mccray PB, Tack B, Jia HP, Schutte BC;

DR WPI; 2002-106302/14.

DR N-PSDB; AAS14407.

XX New human beta-defensin 3 peptides and nucleic acids encoding peptides,

PT useful for treating or preventing microbial growth or infection, or in

PT gene therapy.

XX Claim 1; Page 96; 110pp; English.

CC The present invention relates to the isolation of a novel antimicrobial  
CC peptide, human beta-defensin-3 (HBD-3). Also described is a method of  
CC inhibiting growth of a microbe by introducing into a host or environment  
CC the antimicrobial peptide of the invention. The peptide is useful for  
CC treating or preventing microbial growth or infections, e.g. pulmonary  
CC infections when administered by inhalation. The peptide can be applied on  
CC a work surface or a surgical instrument for the prevention and/or  
CC suppression of microbial growth. The present sequence represents HBD-3

XX SQ Sequence 67 AA;

Query Match 100.0%; Score 65; DB 5; Length 67;

Best Local Similarity 100.0%; Pred. No. 1.9e-60;

Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRIHYLLFALLFLFVPGHGGIINTLQKYYCRVRGRCVAVLSCLPKKEQIGKSTRGR 60

Db 1 MRIHYLLFALLFLFVPGHGGIINTLQKYYCRVRGRCVAVLSCLPKKEQIGKSTRGR 60

QY 61 KCCRR 65

Db 61 KCCRR 65

Db 61 KCCRR 65

RESULT 5

AAU91016

ID AAU91016 standard; peptide; 67 AA.

AC AAU91016;

DT 05-JUN-2002 (first entry)

DE Transplant media associated defensin peptide #17.

XX

XX

XX

KW Transplant; antimicrobial peptide; pore forming agent;  
KW cell surface receptor binding compound; kidney transplant; cardioplegia;  
KW organ transplant; transplant rejection; defensin.

OS Homo sapiens.

PN WO200209738-A1.

PD 07-FEB-2002.

PF 27-JUL-2001; 2001WO-US023785.

PR 28-JUL-2000; 2000US-0221632P.

PR 17-NOV-2000; 2000US-0249602P.

PR 15-MAY-2001; 2001US-0290932P.

XX (MURP/) MURPHY C J.

XX Murphy CJ, Reid TW, Meanlty JF;

XX WPI; 2002-268995/31.

XX Media comprising antimicrobial polypeptides or pore forming agents and/or  
XX cell surface receptor binding compounds useful for the storage and  
XX preservation of organs prior to transplant.

XX Claim 8; Page 28; 78pp; English.

CC The invention describes new transplant compositions comprising  
CC antimicrobial polypeptides or pore forming agents and/or cell surface  
CC receptor binding compounds. The media is capable of extending the  
CC preservation period past 72 hours and can provide organs with increased  
CC functionality upon transplant. animals receiving kidneys stored in the  
CC media of the present invention for either three or four days had serum  
CC creatinine levels of less than half of those observed in control animals  
CC receiving kidneys stored in UW solution (defined in the specification)  
CC alone. Lower serum creatinine levels are indicative of healthier kidneys  
CC and a more preferable prognosis for the transplant patient. The media of  
CC the invention are useful for decreasing the incidence and/or severity of  
CC delayed graft function in patients receiving transplanted kidneys stored  
CC and/or treated in the media. The media may also be used in procedures  
CC such as cardioplegia. It is contemplated that transplant of healthier  
CC organs leads to a decrease in chronic rejection. This sequence represents  
CC an antimicrobial defensin peptide studied in the development of the  
CC transplant media

XX SQ Sequence 67 AA;

Query Match 100.0%; Score 65; DB 5; Length 67;

Best Local Similarity 100.0%; Pred. No. 1.9e-60;

Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRIHYLLFALLFLFVPGHGGIINTLQKYYCRVRGRCVAVLSCLPKKEQIGKSTRGR 60

Db 1 MRIHYLLFALLFLFVPGHGGIINTLQKYYCRVRGRCVAVLSCLPKKEQIGKSTRGR 60

QY 61 KCCRR 65

Db 61 KCCRR 65

Db 61 KCCRR 65

RESULT 6

AAU91036

ID AAU91036 standard; peptide; 67 AA.

AC AAU91036;

DT 05-JUN-2002 (first entry)

DE Transplant media associated defensin peptide #37.

XX

XX

XX

XX

XX

XX

XX

XX

XX

KW Transplant; antimicrobial peptide; pore forming agent;  
KW cell surface receptor binding compound; kidney transplant; cardioplegia;

XX organ transplant; transplant rejection; defensin.  
XX Homo sapiens.  
OS  
XX WO200209738-A1.  
PN  
XX  
XX 07-FEB-2002.  
PD  
XX  
XX 27-JUL-2001; 2001WO-US023785.  
PF  
XX  
XX 28-JUL-2000; 2000US-0221632P.  
PR 17-NOV-2000; 2000US-0249602P.  
PR 15-MAY-2001; 2001US-0290932P.  
XX  
XX (MURP/) MURPHY C J.  
PA  
XX  
XX PI Murphy CJ, Reid TW, Mcanulty JF;  
PI  
XX WPI; 2002-268995/31.  
DR  
XX  
XX Media comprising antimicrobial polypeptides or pore forming agents and/or  
PT cell surface receptor binding compounds useful for the storage and  
PT preservation of organs prior to transplant.  
PT  
XX  
XX Claim 8; Page 30; 78pp; English.  
PS  
XX  
XX The invention describes new transplant compositions comprising  
CC antimicrobial polypeptides or pore forming agents and/or cell surface  
CC receptor binding compounds. The media is capable of extending the  
CC preservation period past 72 hours and can provide organs with increased  
CC functionality upon transplant. animals receiving kidneys stored in the  
CC media of the present invention for either three or four days had serum  
CC creatinine levels of less than half of those observed in control animals  
CC receiving kidneys stored in UW solution (defined in the specification)  
CC alone. Lower serum creatinine levels are indicative of healthier kidneys  
CC and a more preferable prognosis for the transplant patient. The media of  
CC the invention are useful for decreasing the incidence and/or severity of  
CC delayed graft function in patients receiving transplanted kidneys stored  
CC and/or treated in the media. The media may also be used in procedures  
CC such as cardioplegia. It is contemplated that transplant of healthier  
CC organs leads to a decrease in chronic rejection. This sequence represents  
CC an antimicrobial defensin peptide studied in the development of the  
CC transplant media  
CC  
XX  
SQ Sequence 67 AA;  
Query Match 100.0%; Score 65; DB 5; Length 67;  
Best Local Similarity 100.0%; Pred. No. 1.9e-60;  
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MRIHYLLFALLFLFLVPVPGHGIIINTLQKYYCVRGRCAYLSCLPKKEQIGKSTRGR 60  
DB 1 MRIHYLLFALLFLFLVPVPGHGIIINTLQKYYCVRGRCAYLSCLPKKEQIGKSTRGR 60  
QY 61. KCCRR 65  
DB 61 KCCRR 65  
RESULT 7  
AA017768  
ID AA017768 standard; protein; 67 AA.  
XX  
XX AA017768;  
AC  
XX  
XX 30-AUG-2002 (first entry)  
DT  
XX  
XX Human beta-defensin-3 derivative #3.  
DE  
XX  
XX Human; beta-defensin-3; hBD-3; bacterial infection; gene therapy;  
KW respiratory system; cystic fibrosis; inflammation; urogenital tract;  
KW antibacterial; fungicide; cytostatic; antiinflammatory; antitumor;  
KW gastrointestinal tract; septicemia; apoptosis induction; cancer.  
PA

XX Homo sapiens.  
OS  
XX WO200240512-A2.  
PN  
XX  
XX 23-MAY-2002.  
PD  
XX  
XX 14-NOV-2001; 2001WO-EP013174.  
PF  
XX  
XX 14-NOV-2000; 2000DE-01056365.  
PR 30-MAR-2001; 2001DE-01016220.  
PR  
XX  
XX (IPFP-) IPF PHARM GMBH.  
PA  
XX  
XX PI Forssmann W, Kluever E, Conejo-Garcia J, Adermann K, Bals R;  
PI Maegert H;  
XX  
XX WPI; 2002-435959/46.  
DR  
XX  
XX New human beta-defensin 3, useful for treating or preventing microbial  
PT infection and tumors, also related nucleic acid.  
PT  
XX  
XX Claim 2; Page 23; 36pp; German.  
PS  
XX  
XX The present invention relates to human beta-defensin-3 (hBD-3) and its  
CC derivatives. The peptide, its coding sequence and vectors containing the  
CC coding sequence are useful in (gene) therapy and diagnosis, especially  
CC for preventing or treating a wide range of microbial infections  
CC (particularly Burkholderia cepacia and Pseudomonas aeruginosa in the  
CC respiratory tract, especially in cases of cystic fibrosis, and  
CC Helicobacter pylori, also inflammatory diseases of the gastrointestinal  
CC and urogenital tracts, sepsis and yeast infections), and for inducing  
CC apoptosis for treating malignant melanoma and tumours. The present  
CC sequence is a derivative of human BD-3  
CC  
XX  
SQ Sequence 67 AA;  
Query Match 100.0%; Score 65; DB 5; Length 67;  
Best Local Similarity 100.0%; Pred. No. 1.9e-60;  
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MRIHYLLFALLFLFLVPVPGHGIIINTLQKYYCVRGRCAYLSCLPKKEQIGKSTRGR 60  
DB 1 MRIHYLLFALLFLFLVPVPGHGIIINTLQKYYCVRGRCAYLSCLPKKEQIGKSTRGR 60  
QY 61 KCCRR 65  
DB 61 KCCRR 65  
RESULT 8  
ADN05995  
ID ADN05995 standard; protein; 67 AA.  
XX  
XX ADN05995;  
AC  
XX  
XX 01-JUL-2004 (first entry)  
DT  
XX  
XX Antipsoriatic protein sequence #1157.  
DE  
XX  
XX antipsoriatic; gene therapy; psoriasis; diagnosis.  
KW  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO2004028479-A2.  
PN  
XX  
XX 08-APR-2004.  
PD  
XX  
XX 25-SEP-2003; 2003WO-US030907.  
PF  
XX  
XX 25-SEP-2002; 2002US-0414006P.  
PR  
XX  
XX (GETH ) GENENTECH INC.  
PA



XX Bodary S, Clark H, Jackman J, Schoenfeld J, Williams PM, Wood WI;  
PI Wu TD;  
XX WPI; 2004-305105/28.  
DR N-PSDB; ADN05994.  
XX  
PT New PRO nucleic acid or polypeptide, useful for preparing a  
PT pharmaceutical composition for diagnosing or treating psoriasis in a  
PT mammal.  
XX  
PS Claim 9; SEQ ID NO 2390; 3069pp; English.  
XX  
CC The invention relates to novel polynucleotide and polypeptides for  
CC treating psoriasis or a sequence having at least 80% identity to the  
CC above sequences. The nucleic acid is useful for preparing a composition  
CC for diagnosing or treating psoriasis in a mammal. This sequence  
CC corresponds to one of the polypeptides of the invention.  
XX  
SQ Sequence 67 AA;

Query Match 100.0%; Score 65; DB 8; Length 67;  
Best Local Similarity 100.0%; Pred. No. 1.9e-60;  
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MRHYLLFALLFLVLPVPGHGIINTLQKYYCRVRGRCAYLSCLPKEEQIGKCGSTRGR 60  
|||  
1 MRHYLLFALLFLVLPVPGHGIINTLQKYYCRVRGRCAYLSCLPKEEQIGKCGSTRGR 60

OY 61 KCCRR 65  
|||  
61 KCCRR 65

Db 61 KCCRR 65

RESULT 9  
ADQ08006  
ID ADQ08006 standard; protein; 67 AA.

XX ADQ08006;

DT 23-SEP-2004 (first entry)

DE Human beta-defensin-3, HBD-3, SEQ ID 15.

KW Anti-HIV; Vaccine; HIV infection; Beta Defensin; BD; human; HBD; HBD-2;  
HBD-3; antiviral.

OS Homo sapiens.

PN WO2004054603-A2.

PD 01-JUL-2004.

PF 15-DEC-2003; 2003WO-US040233.

PR 13-DEC-2002; 2002US-0433099P.

PA (UYCA-) UNIV CASE WESTERN RESERVE.

PI Weinberg A;

DR WPI; 2004-488004/46.

DR N-PSDB; ADQ08007; ADQ08008, ADQ08009.

XX Inhibiting HIV infection in a subject comprises administering human Beta  
PT defensin-2 or human Beta defensin-3 agent or Beta Defensin-inducing  
PT agent.

PS Claim 9; Page 10; 63pp; English.

XX The present invention relates to a method for inhibiting HIV infection in  
CC a subject. The method comprises administering Beta Defensin (BD) agent or  
CC Beta Defensin-inducing agent e.g. a human BD (HBD) agent such as HBD-2 or

CC HBD-3. The agent is administered in combination with an additional  
CC antiviral agent which targets a portion of the HIV virus consisting of an  
CC HIV protease or an HIV reverse transcriptase. BD are a superfamily of  
CC peptide antibiotics with a characteristic beta-sheet structure stabilised  
CC by two to three intramolecular disulfide bonds. The present sequence is  
CC HBD-3.  
XX  
SQ Sequence 67 AA;

Query Match 100.0%; Score 65; DB 8; Length 67;  
Best Local Similarity 100.0%; Pred. No. 1.9e-60;  
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MRHYLLFALLFLVLPVPGHGIINTLQKYYCRVRGRCAYLSCLPKEEQIGKCGSTRGR 60  
|||  
1 MRHYLLFALLFLVLPVPGHGIINTLQKYYCRVRGRCAYLSCLPKEEQIGKCGSTRGR 60

OY 61 KCCRR 65  
|||  
61 KCCRR 65

Db 61 KCCRR 65

RESULT 10  
AAB10600  
ID AAB10600 standard; protein; 45 AA.

XX AAB10600;

DT 08-JAN-2001 (first entry)

DE Human SAP-3 mature protein.

KW SAP-2; SAP-3; human; antibiotic; antibacterial; antifungal; antiviral;  
treatment; microbial infection; wound dressing; diagnostic reagent.

OS Homo sapiens.

PN WO200046245-A2.

PD 10-AUG-2000.

PF 01-FEB-2000; 2000WO-EP000776.

PR 01-FEB-1999; 99DE-01005128.

PR 08-OCT-1999; 99DE-01049436.

PA (SCHD ) SCHERING AG.

PI Christophers E, Harder J, Schroeder J;

DR WPI; 2000-514948/46.

DR N-PSDB; AAA71753.

XX New human antibiotic peptides, useful for treating microbial infections,  
PT particularly when incorporated in wound dressings, also related nucleic  
PT acid.

PS Claim 1; Page 37; 41pp; German.

XX This invention describes the novel active, mature human proteins (I) SAP-  
CC 2 and SAP-3 which have antibiotic, antibacterial, antifungal and  
CC antiviral activity. (I), and their precursors, are useful for treating or  
CC preventing microbial infections (caused by bacteria, fungi or viruses),  
CC particularly where they (or human cells expressing them) are included in  
CC wound dressings, and to produce specific antibodies (Ab) or their  
CC fragments. Ab are used as diagnostic reagents, e.g. to detect a  
CC deficiency of (I) or the presence of a (I) variant. This sequence  
CC represents the mature human SAP-3 protein described in the method of the  
CC invention

SQ Sequence 45 AA;

Query Match 66.2%; Score 43; DB 3; Length 45;

Best Local Similarity 100.0%; Pred. No. 1.9e-37;  
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 GIINTLQKYYCVRVGRGCAVLSCLPKEEQIGKCGSTRGRKCCRR 65  
Db 1 GIINTLQKYYCVRVGRGCAVLSCLPKEEQIGKCGSTRGRKCCRR 43

RESULT 11

AAU09709 standard; protein, 45 AA.

AAU09709;

26-MAR-2002 (first entry)

Human beta-defensin-3 (HBD-3) mature protein sequence #2.

Human; antimicrobial peptide; human beta-defensin-3; HBD-3;

microbial growth; microbial infection; pulmonary infection.

Homo sapiens.

WO200192309-A2.

06-DEC-2001.

01-JUN-2001; 2001WO-US018057.

01-JUN-2000; 2000US-0208792P.

(IOWA ) UNIV IOWA RES FOUND.

McCray PB, Tack B, Jia HP, Schutte BC;

WPI; 2002-106302/14.

New human beta-defensin 3 peptides and nucleic acids encoding peptides,

useful for treating or preventing microbial growth or infection, or in

gene therapy.

Claim 29; Page 98; 110pp; English.

The present invention relates to the isolation of a novel antimicrobial

peptide, human beta-defensin-3 (HBD-3). Also described is a method of

inhibiting growth of a microbe by introducing into a host or environment

the antimicrobial peptide of the invention. The peptide is useful for

treating or preventing microbial growth or infections, e.g. pulmonary

infections when administered by inhalation. The peptide can be applied on

a work surface or a surgical instrument for the prevention and/or

suppression of microbial growth. The present sequence represents HBD-3

mature protein sequence #2

Sequence 45 AA;

Query Match 66.2%; Score 43; DB 5; Length 45;  
Best Local Similarity 100.0%; Pred. No. 1.9e-37;  
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 GIINTLQKYYCVRVGRGCAVLSCLPKEEQIGKCGSTRGRKCCRR 65  
Db 1 GIINTLQKYYCVRVGRGCAVLSCLPKEEQIGKCGSTRGRKCCRR 43

RESULT 12

AAO17767 standard; peptide, 45 AA.

AAO17767;

30-AUG-2002 (first entry)

Human beta-defensin-3 derivative #2.

XX Human; beta-defensin-3; hBD-3; bacterial infection; gene therapy;  
KW respiratory system; cystic fibrosis; inflammation; urogenital tract;  
KW antibacterial; fungicide; cytostatic; antiinflammatory; antiulcer;  
KW gastrointestinal tract; septicemia; apoptosis induction; cancer.

Homo sapiens.

WO200240512-A2.

23-MAY-2002.

14-NOV-2001; 2001WO-EP013174.

14-NOV-2000; 2000DE-01056365.

30-MAR-2001; 2001DE-01016220.

(IPFP-) IPF PHARM GMBH.

Forssmann W, Kluever E, Corejo-Garcia J, Adermann K, Bals R;

Maeger H;

WPI; 2002-435959/46.

New human beta-defensin 3, useful for treating or preventing microbial

infection and tumors, also related nucleic acid.

Claim 2; Page 23; 36pp; German.

The present invention relates to human beta-defensin-3 (hBD-3) and its

derivatives. The peptide, its coding sequence and vectors containing the

coding sequence are useful in (gene) therapy and diagnosis, especially

for preventing or treating a wide range of microbial infections

(particularly Burkholderia cepacia and Pseudomonas aeruginosa in the

respiratory tract, especially in cases of cystic fibrosis, and

Helicobacter pylori, also inflammatory diseases of the gastrointestinal

tract and urogenital tracts, sepsis and yeast infections), and for inducing

apoptosis for treating malignant melanoma and tumours. The present

sequence is a derivative of human BD-3

Sequence 45 AA;

Query Match 66.2%; Score 43; DB 5; Length 45;  
Best Local Similarity 100.0%; Pred. No. 1.9e-37;  
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 GIINTLQKYYCVRVGRGCAVLSCLPKEEQIGKCGSTRGRKCCRR 65  
Db 1 GIINTLQKYYCVRVGRGCAVLSCLPKEEQIGKCGSTRGRKCCRR 43

RESULT 13

AAU09708 standard; protein, 41 AA.

AAU09708;

26-MAR-2002 (first entry)

Human beta-defensin-3 (HBD-3) mature protein sequence #1.

Human; antimicrobial peptide; human beta-defensin-3; HBD-3;

microbial growth; microbial infection; pulmonary infection.

Homo sapiens.

WO200192309-A2.

06-DEC-2001.

01-JUN-2001; 2001WO-US018057.

01-JUN-2000; 2000US-0208792P.

XX (IOWA ) UNIV IOWA RES FOUND.  
PA Mccray PB, Tack B, Jia HP, Schutte BC;  
XX WPI; 2002-106302/14.  
DR  
XX New human beta-defensin 3 peptides and nucleic acids encoding peptides,  
PT useful for treating or preventing microbial growth or infection, or in  
PT gene therapy.  
XX  
PS Claim 28; Page 97; 110pp; English.  
XX  
CC The present invention relates to the isolation of a novel antimicrobial  
CC peptide, human beta-defensin-3 (HBD-3). Also described is a method of  
CC inhibiting growth of a microbe by introducing into a host or environment  
CC the antimicrobial peptide of the invention. The peptide is useful for  
CC treating or preventing microbial growth or infections, e.g. pulmonary  
CC infections when administered by inhalation. The peptide can be applied on  
CC a work surface or a surgical instrument for the prevention and/or  
CC suppression of microbial growth. The present sequence represents HBD-3  
CC mature protein sequence #1  
XX  
SQ Sequence 41 AA;  
  
Query Match 60.0%; Score 39; DB 5; Length 41;  
Best Local Similarity 100.0%; Pred. No. 2.8e-33;  
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
OY 27 TLQKYCRVRGGRCAYLSCLPKKEQIGKSTRGRKCCR 65  
Db 1 TLQKYCRVRGGRCAYLSCLPKKEQIGKSTRGRKCCR 39  
  
RESULT 14  
AA017766  
ID AA017766 standard; peptide; 40 AA.  
XX  
AC AA017766;  
XX  
DT 30-AUG-2002 (first entry)  
XX  
DE Human beta-defensin-3 derivative #1.  
XX  
XM Human; beta-defensin-3; hBD-3; bacterial infection; gene therapy;  
KM respiratory system; cystic fibrosis; inflammation; urogenital tract;  
KM antibacterial; fungicide; cytostatic; antiinflammatory; antiulcer;  
KM gastrointestinal tract; septicemia; apoptosis induction; cancer.  
XX  
OS Homo sapiens.  
XX  
PN WO200240512-A2.  
XX  
PD 23-MAY-2002.  
XX  
PF 14-NOV-2001; 2001WO-EP013174.  
XX  
PR 14-NOV-2000; 2000DE-01056365.  
PR 30-MAR-2001; 2001DE-01016220.  
XX  
PA (IPFP-) IPF PHARM GMBH.  
XX  
PI Forsmann W, Kluever E, Conejo-Garcia J, Adermann K, Bals R;  
PI Maegerl H;  
XX  
DR WPI; 2002-435959/46.  
XX  
PT New human beta-defensin 3, useful for treating or preventing microbial  
PT infection and tumors, also related nucleic acid.  
XX  
PS Claim 2; Page 23; 36pp; German.  
XX  
CC The present invention relates to human beta-defensin-3 (hBD-3) and its

CC derivatives. The peptide, its coding sequence and vectors containing the  
CC coding sequence are useful in (gene) therapy and diagnosis, especially  
CC for preventing or treating a wide range of microbial infections  
CC (particularly Burkholderia cepacia and Pseudomonas aeruginosa in the  
CC respiratory tract, especially in cases of cystic fibrosis, and  
CC Helicobacter pylori, also inflammatory diseases of the gastrointestinal  
CC and urogenital tracts, sepsis and yeast infections), and for inducing  
CC apoptosis for treating malignant melanoma and tumours. The present  
CC sequence is a derivative of human BD-3  
XX  
SQ Sequence 40 AA;  
  
Query Match 58.5%; Score 38; DB 5; Length 40;  
Best Local Similarity 100.0%; Pred. No. 3.1e-32;  
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
OY 28 LQKYCRVRGGRCAYLSCLPKKEQIGKSTRGRKCCR 65  
Db 1 LQKYCRVRGGRCAYLSCLPKKEQIGKSTRGRKCCR 38  
  
RESULT 15  
ABR43502  
ID ABR43502 standard; peptide; 35 AA.  
XX  
AC ABR43502;  
XX  
DT 16-JUL-2003 (first entry)  
XX  
DE Human beta-defensin peptide DEFB3 SEQ ID NO:7.  
XX  
KM Beta-defensin; antimicrobial; antibacterial; vaccine; gene therapy;  
KM infection; antibiotic; chromosome 8p23-p22.  
XX  
OS Homo sapiens.  
XX  
PN WO2003024992-A2.  
XX  
PD 27-MAR-2003.  
XX  
PF 23-SEP-2002; 2002WO-US030106.  
XX  
PR 21-SEP-2001; 2001US-0323991P.  
XX  
PA (IOWA ) UNIV IOWA RES FOUND.  
XX  
PI Mccray PB, Schutte BC, Jia HP, Casavant TL, Welch MJ;  
XX  
DR WPI; 2003-354585/33.  
XX  
PT New antimicrobial peptides, beta-defensin, useful for preventing  
PT microbial growth, for treating pulmonary infections, for reducing  
PT resistance to antimicrobials and antibiotics, and for inhibiting  
PT multidrug resistant bacteria.  
XX  
PS Claim 1; Page 78; 125pp; English.  
XX  
CC ABR43496 to ABR43577 represent beta-defensin antimicrobial peptides (I).  
CC (I) have antibacterial activity and can be used in vaccines, and in gene  
CC therapy. (I) can be used for preventing microbial growth, for treating  
CC infections (e.g. pulmonary infections), for reducing resistance to  
CC antimicrobials and antibiotics, and for inhibiting multidrug resistant  
CC bacteria. The antimicrobial peptides may be included in food  
CC preparations, pharmaceutical preparations, medicinal and pharmaceutical  
CC products, cosmetic products, hygienic products, cleaning products and  
CC cleaning agents, as well as to any material to which the peptides could  
CC be sprayed on or adhered to where inhibition of microbial growth on such  
CC material is desired. The antimicrobial peptides and nucleic acids  
CC encoding them may be used in gene therapy. ABR43578 to ABR43610 represent  
CC human beta-defensin peptides given in an example from the present  
CC invention  
XX  
SQ Sequence 35 AA;

Query Match 53.8%; Score 35; DB 6; Length 35;  
Best Local Similarity 100.0%; Pred. No. 3.9e-29;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 YYCRVRRGRCVLSCLPKEEQIGKSTRGRKCCR 65  
Db 1 YYCRVRRGRCVLSCLPKEEQIGKSTRGRKCCR 35

Search completed: October 13, 2004, 14:57:06  
Job time : 162 secs